

GenCore version 5.1.6  
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(protein - protein search, using sw model)

on: September 13, 2003, 14:32:07; Search time 53.6667 Seconds  
(without alignments)  
351.959 Million cell updates/sec

tle: US-09-786-260-1

fect score: 644

quence: 1 MKVLISLLLLPLMLMSV.....SRACQFLKQCQLRSFALPL 119

oring table: BLOSUM62

Gapop 10.0, Gapext 0.5

arched: 1107863 seqs, 158726573 residues

tal number of hits satisfying chosen parameters: 1107863

imum DB seq length: 0

imum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

A\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	644	100.0	119	21 AAB34728 Human secreted pro
2	644	100.0	119	21 AAY82453 Human TGC-440 secr
3	644	100.0	119	21 AAY87317 Human signal pepti
4	644	100.0	119	21 AAU66668 Membrane-bound pro
5	644	100.0	119	22 AAU29093 Human PRO polypept
6	644	100.0	119	22 AAG63977 Amino acid sequenc
7	644	100.0	119	22 AAB87538 Human PRO842. Hom
8	644	100.0	119	22 AAB65191 Human PRO842 (UNQ4
9	644	100.0	119	23 ABP54931 Human cytokine PRO

10	644	100.0	119	23 AAG95863 Human secreted/tra
11	644	100.0	119	24 ABU71181 Human PRO842 prote
12	644	100.0	119	24 ABU71518 Human secreted pol
13	644	100.0	119	24 ABU71964 Novel human secret
14	644	100.0	119	24 ABU72121 Human PRO polypept
15	644	100.0	119	24 ABU65638 Human secreted/tra
16	644	100.0	119	24 ABU65971 Novel human secret
17	644	100.0	119	24 ABU67475 Human secreted/tra
18	644	100.0	119	24 ABU65333 Human PRO polypept
19	644	100.0	119	24 ABU59084 Novel human secret
20	644	100.0	119	24 ABU59231 Human secreted/tra
21	644	100.0	119	24 ABU59380 Novel human secret
22	644	100.0	119	24 ABU60515 Human secreted/tra
23	644	100.0	119	24 ABU58006 Human PRO polypept
24	644	100.0	119	24 ABU58469 Human PRO polypept
25	644	100.0	119	24 ABU58937 Human secreted/tr
26	644	100.0	119	24 ABU56005 Human secreted/tra
27	644	100.0	119	24 ABU57000 Human PRO polypept
28	644	100.0	119	24 ABU13897 Human PRO842 polyp
29	644	100.0	119	24 ABU10579 Human secreted/tra
30	644	100.0	119	24 ABU10852 Human PRO polypept
31	548	85.1	97	21 AAY82454 Mature human TGC-4
32	527	81.8	93	19 AAW83953 Polypeptide encode
33	456	70.8	119	21 AAY82457 Mature TGC-440 secr
34	386	59.9	97	21 AAY82458 Rat TGC-440 secret
35	386	59.9	119	21 AAY82455 Human 5' EST secre
36	358	55.6	69	20 AAY11732 Mature rat TGC-440
37	342	53.1	97	21 AAY82456 Human secreted pro
38	296	46.0	64	19 AAW83938 Human 5' EST secre
39	225	34.9	48	20 AAY11731 Propionibacterium
40	78.5	12.2	191	22 AAW66308 Part of chick vita
41	73.5	11.4	70	10 AAP91996 Chicken vitamin D
42	73.5	11.4	70	14 AAR43657 Arabidopsis thalia
43	71.5	11.1	108	23 AAQ21337 Novel human diagno
44	71	11.0	330	22 ABG25331 Human laminin B2 C
45	71	11.0	1798	19 AAW50896

#### ALIGNMENTS

RESULT 1  
AAB34728  
ID AAB34728 standard; Protein; 119 AA.  
XX  
AC AAB34728;  
XX  
DT 26-JAN-2001 (first entry)  
XX  
DE Human secreted protein encoded by DNA clone vq8 1.  
XX  
DE Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;  
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;  
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;  
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;  
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;  
KW psoriasis.  
XX  
OS Homo sapiens  
XX  
PN WO200055375-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-US07285.  
XX  
PR 17-MAR-1999; 99US-0124808.  
XX  
PR 17-MAR-1999; 99US-0124916.  
XX  
PR 17-AUG-1999; 99US-0149639.  
XX  
PR 01-OCT-1999; 99US-0157247.  
XX  
PR 29-NOV-1999; 99US-0167824.  
XX  
PR 15-FEB-2000; 2000US-0182711.  
XX

(ALPH-) ALPHAGENE INC.

Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

WPI: 2000-638211/61.

N-PSDB; AAC59829.

Novel proteins and polypeptides useful for the treatment of e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers

Claim 92; Page 441-442; 493pp; English.

This invention relates to 59 human secreted proteins and the nucleotide sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745 represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59847-C59596. The proteins exhibit neuroprotective, dermatological, immunosuppressive, antiinflammatory, antianemic, nootropic, antiparkinsonian, cerebroprotective, haemostatic, vulnery, cyostatic, antipsoriatic, antibacterial, virucide, and fungicide activity. The proteins and nucleotide sequences are useful as nutritional sources or supplements and in research. The proteins are useful for treating immune deficiency and disorders, which may be genetic or resulting from infections, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis and for treating myeloid or lymphoid cell deficiencies such as anaemias by regulating haemopoiesis. The proteins are also useful in compositions for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, for wound healing, tissue repair and replacement and in the treatment of wounds, incisions and ulcers. Other uses include in the treatment of central and peripheral nervous system and neuropathies such as Alzheimer's and Parkinson's diseases and Shy-Drager syndrome, and mechanical and traumatic disorders, such as spinal cord disorders, head trauma and stroke. The proteins may also be used as a contraceptive, and for treating coagulation disorders such as haemophilias. The protein and nucleotide sequences with cadherin activity are useful for treating cancer. Other uses for the protein include for inhibiting the growth, infection or function of, or killing, infectious agents such as bacteria, virus, fungi and other parasites, for effecting bodily characteristics such as height, weight, hair colour, effecting biorhythms or cardiac cycles or rhythms, effecting metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors, effecting behavioural characteristics, providing analgesic effects and for treating hyperproliferative disorders such as psoriasis.

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 21; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60  
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60  
61 RRKFTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119  
61 RRKFTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119

RESULT 2

AY82453

AY82453 standard; Protein; 119 AA.

AY82453;

30-JUN-2000 (first entry)

Human TGC-440 secretory protein SEQ ID NO:1.

XX TGC-440; secretory protein; immunological disease; infectious disease;  
KW pulmonary function disorder; hepatic function disorder; nephrotropic;  
KW gastrointestinal function disorder; antiinflammatory; immunomodulatory;  
KW virucide; hepatotropic; antiasthmatic; antibacterial; vaccine;  
KW hepatitis; nephritis; influenza; asthma; pulmonary hypertension;  
KW pneumonia; Helicobacter pylori infection.

OS Homo sapiens.

XX WO200014226-A1.

XX 16-MAR-2000.

XX 02-SEP-1999; 99WO-JP04765.

XX 03-SEP-1998; 98JP-0250108.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Ogi K, Tanaka H, Kitada C;

XX WPI: 2000-256978/22.

XX N-PSDB; AAA08343; AAA08344.

Secretory protein TGC440, antibodies to it and compounds promoting or inhibiting its activity for diagnosis and treatment of diseases of the immune system, lung, kidney, liver and intestinal system

Claim 1; Fig 1; 86pp; Japanese.

The present sequence represents a human secretory protein designated TGC-440. TGC-440 has antiinflammatory, nephrotropic, immunomodulatory, virucide, hepatotropic, antiasthmatic and antibacterial activities, and can be used in vaccines. TGC-440 and the polynucleotide sequence encoding it can be used to treat, prevent and diagnose immunological, lung, liver, kidney or gastrointestinal disorders and infectious diseases, such as hepatitis, nephritis, influenza, asthma, pneumonia, pulmonary hypertension, and Helicobacter pylori infection. An antibody immunospecific for TGC-440 is also useful in the above treatment and diagnosis, and also for quantifying the amount of TGC-440 in a liquid specimen.

XX Sequence 119 AA;

Query Match 100.0%; Score 644; DB 21; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

QY 61 RRKFTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119

DB 61 RRKFTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119

RESULT 3

AY87317

ID AY87317 standard; Protein; 119 AA.

XX AY87317;

XX 11-MAY-2000 (first entry)

Human signal peptide containing protein HSPP-94 SEQ ID NO:94.

Human; signal peptide-containing protein; HSPP; diagnosis; cancer;  
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;  
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;  
KW reproductive disorder; developmental disorder; arteriosclerosis;

cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
Parkinson's disease; Huntington's diseases; ovulatory defect;  
muscular dystrophy.

Homo sapiens.

WO200000610-A2.

06-JAN-2000.

25-JUN-1999; 99WO-US14484.

26-JUN-1998; 98US-0090762.

31-JUL-1998; 98US-0094983.

01-OCT-1998; 98US-0102886.

11-DEC-1998; 98US-0112129.

(INCY-) INCYTE PHARM INC.

Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
Bandman O;

WPI: 2000-160673/14.  
N-FSDB; AAZ98202.

New human signal peptide-containing proteins useful in treatment,  
prevention and diagnosis of e.g. cancer, inflammation and  
cardiovascular disease

Claim 1; Page 220-221; 327pp; English.

AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the  
human signal peptide-containing proteins HSPp-1 to HSPp-134. HSPps have  
anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,  
neuroprotective, cardiovascular and antiasthmatic activities, and can  
be used in gene therapy. HSPps can be used to treat or prevent disorders  
associated with decreased activity or function of HSPp. Antagonists of  
HSPp are used to treat or prevent disorders associated with increased  
activity or function of HSPp. Such diseases include cell proliferation  
(including cancer), inflammation, cardiovascular, neurological,  
reproductive or developmental disorders, (e.g. arteriosclerosis,  
cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
asthma, Crohn's disease, microbial or other infections, congestive or  
ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPp  
nucleic acids can be used for the recombinant production of HSPp, for  
detecting HSPp in standard hybridisation and amplification assays (for  
diagnosis and monitoring), in gene therapy, as antisense,  
triplex-forming or ribozyme therapeutics, for detecting related sequences  
or genetic variations, and for chromosomal mapping. HSPp are also used to  
raise specific antibodies (Ab) and to screen for agonists and  
antagonists (potential therapeutic agents). Ab are used to diagnose, or  
monitor, HSPp-related diseases (in usual immunoassays), as therapeutic  
antagonists, in competitive drug screens, and for purification of HSPp  
from natural sources.

Sequence 119 AA:

Query Watch 100.08; Score 644; DB 21; Length 119;  
Best Local Similarity 100.08; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDQGASRRWLQGGQCECKDWFRLAP 60

61 RRKFTVSLPKKQPCDHFHKGNGVKKRPHQRHHRKPNKHSRACQFLKQCLRSFALPL 119

61 RRKFTVSLPKKQPCDHFHKGNGVKKRPHQRHHRKPNKHSRACQFLKQCLRSFALPL 119

RESULT 4

AAV66668

ID AAV66668 standard; protein; 119 AA.

XX AC AAV66668;

XX DT 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO842.

XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

XX KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX PN WO9963088-A2.

XX PD 09-DEC-1999.

XX PF 02-JUN-1999; 99WO-US12252.

XX PR 02-JUN-1998; 98US-0087607.

XX PR 02-JUN-1998; 98US-0087609.

XX PR 02-JUN-1998; 98US-0087759.

XX PR 03-JUN-1998; 98US-0087827.

XX PR 04-JUN-1998; 98US-0088021.

XX PR 04-JUN-1998; 98US-0088025.

XX PR 04-JUN-1998; 98US-0088028.

XX PR 04-JUN-1998; 98US-0088029.

XX PR 04-JUN-1998; 98US-0088030.

XX PR 04-JUN-1998; 98US-0088033.

XX PR 04-JUN-1998; 98US-0088326.

XX PR 05-JUN-1998; 98US-0088167.

XX PR 05-JUN-1998; 98US-0088202.

XX PR 05-JUN-1998; 98US-0088212.

XX PR 05-JUN-1998; 98US-0088217.

XX PR 09-JUN-1998; 98US-0088655.

XX PR 10-JUN-1998; 98US-0088722.

XX PR 10-JUN-1998; 98US-0088730.

XX PR 10-JUN-1998; 98US-0088734.

XX PR 10-JUN-1998; 98US-0088738.

XX PR 10-JUN-1998; 98US-0088740.

XX PR 10-JUN-1998; 98US-0088741.

XX PR 10-JUN-1998; 98US-0088742.

XX PR 10-JUN-1998; 98US-0088810.

XX PR 10-JUN-1998; 98US-0088811.

XX PR 10-JUN-1998; 98US-0088825.

XX PR 10-JUN-1998; 98US-0088826.

XX PR 11-JUN-1998; 98US-0088858.

XX PR 11-JUN-1998; 98US-0088861.

XX PR 11-JUN-1998; 98US-0088863.

XX PR 11-JUN-1998; 98US-0088876.

XX PR 12-JUN-1998; 98US-0089090.

XX PR 12-JUN-1998; 98US-0089105.

XX PR 16-JUN-1998; 98US-0089440.

XX PR 16-JUN-1998; 98US-0089512.

XX PR 16-JUN-1998; 98US-0089514.

XX PR 17-JUN-1998; 98US-0089532.

XX PR 17-JUN-1998; 98US-0089538.

XX PR 17-JUN-1998; 98US-0089598.

XX PR 17-JUN-1998; 98US-0089599.

XX PR 17-JUN-1998; 98US-0089600.

XX PR 17-JUN-1998; 98US-0089653.

XX PR 18-JUN-1998; 98US-0089801.

XX PR 18-JUN-1998; 98US-0089907.

XX PR 18-JUN-1998; 98US-0089908.

XX PR 19-JUN-1998; 98US-0089947.

XX PR 19-JUN-1998; 98US-0089948.

XX PR 19-JUN-1998; 98US-0089952.

XX PR 22-JUN-1998; 98US-0090246.

XX PR 22-JUN-1998; 98US-0090252.

XX PR 22-JUN-1998; 98US-0090254.

23-JUN-1998; 98US-0090349.  
23-JUN-1998; 98US-0090355.  
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24-JUN-1998; 98US-0090435.  
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09-JUL-1998; 98US-0092182.  
10-JUL-1998; 98US-0092472.  
20-JUL-1998; 98US-0093339.  
30-JUL-1998; 98US-0094651.  
04-AUG-1998; 98US-0095282.  
04-AUG-1998; 98US-0095285.  
04-AUG-1998; 98US-0095301.  
04-AUG-1998; 98US-0095302.  
04-AUG-1998; 98US-0095318.  
04-AUG-1998; 98US-0095321.  
04-AUG-1998; 98US-0095325.  
10-AUG-1998; 98US-0095916.  
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10-AUG-1998; 98US-0096012.  
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18-AUG-1998; 98US-0097022.  
19-AUG-1998; 98US-0097141.  
20-AUG-1998; 98US-0097218.  
24-AUG-1998; 98US-0097661.  
26-AUG-1998; 98US-0097951.  
26-AUG-1998; 98US-0097952.

26-AUG-1998; 98US-0097954.  
26-AUG-1998; 98US-0097955.  
26-AUG-1998; 98US-0097971.  
26-AUG-1998; 98US-0097974.  
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26-AUG-1998; 98US-0097985.  
26-AUG-1998; 98US-0098014.  
31-AUG-1998; 98US-0098525.  
16-SEP-1998; 98US-0100634.  
12-JAN-1999; 98US-0115565.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
XX WPI; 2000-072883/06.  
DR N-PSDB; AA265001.  
XX  
XX Membrane-bound proteins and related nucleotide sequences  
XX  
XX claim 12; Fig 99; 822pp; English.  
XX  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
XX Sequence 119 AA;  
SQ  
Query Match 100.0%; Score 644; DB 21; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRGQASRRWLQGGQCECKDWFLRAP 60  
Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRGQASRRWLQGGQCECKDWFLRAP 60  
QY 61 RRKFTVSGLPKKQPCDHFHFGKGNVKKTRHQRHRRKPNKHSRACQOFLKQCQLRSPALPL 119  
Db 61 RRKFTVSGLPKKQPCDHFHFGKGNVKKTRHQRHRRKPNKHSRACQOFLKQCQLRSPALPL 119  
RESULT 5  
AAU29093  
ID AAU29093 standard; Protein; 119 AA.  
XX  
XX AAU29093;  
XX  
XX 18-DEC-2001 (first entry)  
XX  
XX Human PRO polypeptide sequence #70.  
XX  
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200168848-A2.  
XX  
XX

subjects. The orthogonal

can be used for genetic analysis of individuals with genetic disorders.

XX Sequence 119 AA; Query Match 100.0%; Score 644; DB 22; Length 119;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-66; Indels 0; Gaps 0;  
 XX Matches 119; Conservative 0; Mismatches 0;

1 MKVLISLILLPLMLMSYSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFLRAP 60  
 1 MKVLISLILLPLMLMSYSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFLRAP 60

61 RRKFTWVGLPKKQCPDHFKNVKKTRHORHHRKKNKHSRACQQLKOCQLRSFALPL 119  
 61 RRKFTWVGLPKKQCPDHFKNVKKTRHORHHRKKNKHSRACQQLKOCQLRSFALPL 119

RESULT 6  
 AAG63977 standard; Protein: 119 AA.  
 XX AAG63977;  
 XX AC  
 XX DT  
 XX (first entry)  
 XX 13-NOV-2001 (first entry)  
 XX Amino acid sequence of a human Lng104 polypeptide.  
 DE Human; lung cancer specific gene; LSG; Lng104; lung cancer.  
 KW Homo sapiens.  
 OS WO200161055-A2.  
 PN 23-AUG-2001.  
 PD 20-FEB-2001; 2001WO-US05674.  
 XX 17-FEB-2000; 2000US-0183188.  
 XX {DIAD-} DIADEXUS INC.  
 PA Chen S, Sun Y, Macina RA;  
 PI WPI: 2001-529917/58.  
 DR N-PSDB; AAH77949, AAH77951.  
 XX New lung cancer specific gene for the treatment and diagnosis of lung  
 PT cancer -  
 PS Claim 2; Page 115-116; 119pp; English.  
 XX The present sequence is encoded by a human lung cancer specific gene  
 XX (LSG), and represents a polypeptide designated Lng104. LSGs are useful  
 XX in the treatment and diagnosis of lung cancer. The treatment of lung  
 XX cancer comprises the administration of a molecule which down regulates  
 XX the expression of an LSG. An immune response can be mounted against a  
 XX target cell expressing an LSG. Identification of potential therapeutic  
 XX agents for use in imaging and treating lung cancer which comprises  
 XX of an LSG relative to LSG in the absence of the agent where the ability  
 XX of a molecule to bind to the LSG or decrease expression of the LSG is  
 XX indicative of the molecule being useful in imaging and treating lung  
 XX cancer.

XX Sequence 119 AA;  
 XX Query Match 100.0%; Score 644; DB 22; Length 119;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
 XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLILLPLMLMSYSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFLRAP 60  
 1 MKVLISLILLPLMLMSYSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFLRAP 60

61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119  
|||||  
61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119  
|||||

SUIT 7  
B87538  
AAB87538 standard; Protein; 119 AA.  
AAB87538;

15-MAY-2001 (first entry)  
Human PRO842.  
Human; PRO protein; mapping.  
Homo sapiens.

WO200116318-A2.  
08-MAR-2001.

24-AUG-2000; 2000WO-US23328.  
01-SEP-1999; 99WO-US20111.  
15-SEP-1999; 99WO-US21090.  
07-DEC-1999; 99US-0169495.  
09-DEC-1999; 99US-0170462.  
11-JAN-2000; 2000US-0175481.  
18-FEB-2000; 2000WO-US04341.  
18-FEB-2000; 2000WO-US04342.  
22-FEB-2000; 2000WO-US04414.  
01-MAR-2000; 2000WO-US05601.  
03-MAR-2000; 2000US-0187202.  
25-APR-2000; 2000US-0199397.  
22-MAY-2000; 2000WO-US14042.  
05-JUN-2000; 2000US-0209832.

(GETH ) GENENTECH INC.  
Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
WPI: 2001-183260/18.  
N-PSDB; AAF92070.  
Eighty four nucleic acids encoding PRO polypeptides, useful in  
molecular biology, including use as hybridization probes, and in  
chromosome and gene mapping.  
Claim 12; Fig 26; 278pp; English.

The present sequence is a human PRO polypeptide (secreted and  
transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
anti-PRO antibodies are useful for preparation of a medicament useful in  
the treatment of a condition which is responsive to the PRO protein,  
agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
employed as molecular weight markers for protein electrophoresis. The PRO  
coding sequence has applications in molecular biology, including use as  
hybridisation probes, and in chromosome and gene mapping.

Sequence 119 AA;  
Query Match 100.0%; Score 644; DB 22; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDGOASRRWLQEGQCECKDWFRLAP 60  
|||||  
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDGOASRRWLQEGQCECKDWFRLAP 60  
|||||

QY 61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119  
|||||  
Db 61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119  
|||||

RESULT 8  
AAB65191  
X X AAB65191 standard; Protein; 119 AA.  
X X AAB65191;  
X X  
Dt 02-APR-2001 (first entry)  
X X Human PRO842 (UNQ473) protein sequence SEQ ID NO:165.

X X Human; secreted and transmembrane protein; PRO; cytostatic;  
K W cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
K W diagnostic assay.

X X Homo sapiens.  
X X WO200073454-A1. — US 661  
X X  
X X 07-DEC-2000.

X X 30-MAR-2000; 2000WO-US08439.  
X X  
X X 02-JUN-1999; 99WO-US12252.  
X X 23-JUN-1999; 99US-0141037.  
X X 07-JUL-1999; 99US-0143048.  
X X 20-JUL-1999; 99US-0144758.  
X X 26-JUL-1999; 99US-0145698.  
X X 28-JUL-1999; 99US-0146222.  
X X 17-AUG-1999; 99US-0149396.  
X X 15-SEP-1999; 99WO-US21090.  
X X 15-SEP-1999; 99WO-US21347.  
X X 08-OCT-1999; 99US-0158663.  
X X 30-NOV-1999; 99WO-US28313.  
X X 01-DEC-1999; 99WO-US28301.  
X X 16-DEC-1999; 99WO-US30095.  
X X 20-DEC-1999; 99WO-US30911.  
X X 05-JAN-2000; 2000WO-US00219.  
X X 06-JAN-2000; 2000WO-US00376.  
X X 11-FEB-2000; 2000WO-US03565.  
X X 18-FEB-2000; 2000WO-US04341.  
X X 22-FEB-2000; 2000WO-US04414.  
X X 24-FEB-2000; 2000WO-US04914.  
X X 24-FEB-2000; 2000WO-US05004.  
X X 02-MAR-2000; 2000WO-US05841.  
X X 15-MAR-2000; 2000WO-US06884.  
X X 20-MAR-2000; 2000WO-US07377.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi CJ, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;

WPI: 2001-032160/04.  
N-PSDB; AAF44147.

PRO polynucleotides used to produce polypeptides used to target  
bioactive molecules such as toxins, radiolabels or antibodies, to  
specific cells, to cause targeted cell death -

Claim 12; Fig 99; 935pp; English.

The present invention describes human secreted and transmembrane PRO  
proteins. The PRO proteins have cytostatic activity. The PRO proteins  
can be used for targeted delivery of bioactive molecules, such as  
toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44289 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 22; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60  
 |||||  
 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60  
 |||||  
 61 RRKFTMTVSGLPKQCCDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119  
 |||||  
 61 RRKFTMTVSGLPKQCCDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

SULT 9

P54931  
 ABP54931 standard; Protein; 119 AA.

ABP54931;

08-JAN-2003 (first entry)

Human cytokine PRO842 (CK27).

PRO842; CK27; chemokine; human; antiinflammatory; dermatological;  
 hepatotropic; anti-allergic; antiasthmatic; immunosuppressive;  
 antithyroid; antidiabetic; antianaemic; haemostatic; antipsoriatic;  
 antirheumatic; antiarthritic; nephrotropic.

Homo sapiens.

Key Location/Qualifiers  
 Peptide 1..22  
 /label= Signal\_peptide  
 Protein 23..119  
 /label= Mature\_protein  
 Modified-site 27..32  
 /note= "potential N-myristoylation site"  
 Modified-site 39..41  
 /note= "potential protein kinase C phosphorylation site"  
 Modified-site 46..51  
 /note= "potential N-myristoylation site"

WO200270706-A2.

12-SEP-2002.

07-DEC-2001; 2001WO-US48060.

28-FEB-2001; 2001WO-US06520.

28-AUG-2001; 2001US-0941992.

(GENTECH ) GENENTECH INC.

French D, Grimaldi JC, Hillan KJ, Pisabarro MT, Schmidt KN;

Smith V, Tumas D, Vandlen RL, Watanabe CK, Williams PM, Wood WI;

WPI: 2002-750461/81.

N-PSDB; ABV73914.

PT New PRO842 polypeptides having structural homology to interleukin-8,  
 PT useful for treating or diagnosing a mammal with an inflammatory disease  
 PT or immune related disease, e.g. rheumatoid arthritis, osteoarthritis or  
 PT allergic disease  
 XX  
 XX  
 XX  
 PS Claim 1; Fig 2; 118pp; English.

CC The present sequence is the protein sequence of PRO842 (CK27),  
 CC a novel human chemokine (mol.wt. 13.8 kDa, pI 11.16) having  
 CC structural homology to interleukin-8. Microarray analysis has  
 CC shown PRO842 to be over-expressed in colon tumour, lung tumour and  
 CC breast tumour cells compared with non-cancerous human tissue,  
 CC making it a useful diagnostic marker for cancerous tumours and a  
 CC therapeutic target. PRO842 also plays a role in the inflammatory  
 CC response, having chemoattractant properties toward monocytes and  
 CC dendritic cells. The invention provides PRO842 polypeptides,  
 CC polynucleotides, host cells, vectors and antibodies, as well as  
 CC methods of treating an immune related disorder by using a PRO842  
 CC polypeptide, or an agonist, antagonist or antibody. The immune  
 CC related disorder may be systemic lupus erythematosus, rheumatoid  
 CC arthritis, osteoarthritis, juvenile chronic arthritis,  
 CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory  
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,  
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,  
 CC demyelinating disease of the central or peripheral nervous system,  
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
 CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary  
 CC disease, infectious or autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
 CC disease, an autoimmune or immune-mediated skin disease, a bullous  
 CC skin disease, erythema multiforme, contact dermatitis, psoriasis,  
 CC an allergic disease, asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity, urticaria, an immunologic disease of the  
 CC ovaries, an immunologic disease of the lung, eosinophilic  
 CC pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
 CC pneumonitis, a transplantation associated disease, graft rejection  
 CC or graft-versus-host-disease (all claimed).

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 23; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60  
 |||||  
 Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60  
 |||||  
 QY 61 RRKFTMTVSGLPKQCCDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119  
 |||||  
 Db 61 RRKFTMTVSGLPKQCCDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

RESULT 10

ABG95863

ID ABG95863 standard; Protein; 119 AA.

XX AC ABG95863;

XX DT 10-DEC-2002 (first entry)

XX DE Human secreted/transmembrane protein PRO842.

XX KW Human; secreted protein; transmembrane protein; antirheumatic;

XX KW antiarthritic; osteopathic; sports-related joint problem;

XX KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX OS Homo sapiens.

XX PN US2002119130-A1.

XX

29-AUG-2002.  
 06-DEC-2001; 2001US-0006867.  
 29-OCT-1997; 97US-063435P.  
 29-OCT-1997; 97US-064215P.  
 22-APR-1998; 98US-082797P.  
 29-APR-1998; 98US-083495P.  
 15-MAY-1998; 98US-085579P.  
 10-JUN-1998; 98US-088811P.  
 10-JUN-1998; 98US-088824P.  
 10-JUN-1998; 98US-088825P.  
 11-JUN-1998; 98US-088863P.  
 12-JUN-1998; 98US-089105P.  
 16-JUN-1998; 98US-089514P.  
 08-SEP-1998; 98WO-US19330.  
 16-MAR-1999; 99WO-US05028.  
 14-MAY-1999; 99WO-US10733.  
 02-JUN-1999; 99WO-US12252.  
 01-SEP-1999; 99WO-US20111.  
 15-SEP-1999; 99WO-US21090.  
 15-SEP-1999; 99WO-US21194.  
 22-DEC-1999; 99WO-US07020.  
 18-FEB-2000; 2000WO-US04341.  
 18-FEB-2000; 2000WO-US04342.  
 30-MAR-2000; 2000WO-US08439.  
 22-MAY-2000; 2000WO-US14042.  
 02-JUN-2000; 2000WO-US15264.  
 23-AUG-2000; 2000WO-US23522.  
 24-AUG-2000; 2000WO-US23328.  
 10-NOV-2000; 2000WO-US30873.  
 01-DEC-2000; 2000WO-US32378.  
 20-DEC-2000; 2000WO-US34956.  
 28-FEB-2001; 2001WO-US06520.  
 20-JUN-2001; 2001WO-US19692.  
 29-JUN-2001; 2001WO-US21066.  
 09-JUL-2001; 2001WO-US21735.  
 (GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI: 2002-731348/79.  
 N-PSDB; ABS74390.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis

Claim 20; Fig 26; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG5851-ABG5934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a

polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, and as articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence represents a novel secreted or transmembrane protein of the invention.

XX Sequence 119 AA;

Query Match 100.0%; Score 644; DB 23; Length 119;

Best Local Similarity 100.0%; Pred. No. 1.8e-66; Indels 0; Gaps 0;  
 Matches 119; Conservative 0; Mismatches 0;

QY 1 MKVLISLILLPLMLSMVSSSLNPGVARGHRDRGQASRRMLQEGGCECKDWFLRAP 60

||||| 1 MKVLISLILLPLMLSMVSSSLNPGVARGHRDRGQASRRMLQEGGCECKDWFLRAP 60

QY 61 RRKPTVSGLPKKQCCDHFPGKGNVKTTRQHRHKNKHSRACQFLKCCQLRSFALPL 119

||||| 61 RRKPTVSGLPKKQCCDHFPGKGNVKTTRQHRHKNKHSRACQFLKCCQLRSFALPL 119

DB 61 RRKPTVSGLPKKQCCDHFPGKGNVKTTRQHRHKNKHSRACQFLKCCQLRSFALPL 119

||||| 61 RRKPTVSGLPKKQCCDHFPGKGNVKTTRQHRHKNKHSRACQFLKCCQLRSFALPL 119

RESULT 11

ABU71181 ID ABU71181 standard; Protein; 119 AA.

XX AC ABU71181;

XX DT 10-JUN-2003 (first entry)

XX DE Human PRO842 protein.

XX KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;  
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;  
 KW differentiation; tumour; gene therapy.

XX OS Homo sapiens.

XX PN US2003036143-A1.

XX PD 20-FEB-2003.

XX PF 02-JUL-2002; 2002US-0187600.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 14-MAY-1999; 99WO-US10733.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 02-DEC-1999; 99WO-US28551.

XX PR 30-DEC-1999; 99WO-US31274.

XX PR 05-JAN-2000; 2000WO-US00219.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 18-FEB-2000; 2000WO-US04342.

XX PR 22-FEB-2000; 2000WO-US04414.





18-AUG-1998; 98US-096949P.  
18-AUG-1998; 98US-096959P.  
18-AUG-1998; 98US-097022P.  
26-AUG-1998; 98US-097952P.  
26-AUG-1998; 98US-097954P.  
26-AUG-1998; 98US-097955P.  
26-AUG-1998; 98US-097971P.  
26-AUG-1998; 98US-097974P.  
26-AUG-1998; 98US-098014P.  
01-SEP-1998; 98US-098716P.  
01-SEP-1998; 98US-098723P.  
02-SEP-1998; 98US-098803P.  
02-SEP-1998; 98US-098821P.  
02-SEP-1998; 98US-098843P.  
09-SEP-1998; 98US-099602P.  
10-SEP-1998; 98US-099741P.  
10-SEP-1998; 98US-099754P.  
10-SEP-1998; 98US-099763P.  
10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 644; DB 24; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKYLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRMLQEGGQCECKDWFLRAP 60  
1 MKYLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRMLQEGGQCECKDWFLRAP 60  
61 RRKFMVTYSGLPKKQPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119  
61 RRKFMVTYSGLPKKQPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119

SUITE 12

ABU71518 standard; Protein; 119 AA.

ABU71518;

10-JUN-2003 (first entry)

Human secreted polypeptide PRO842.

Human; gene therapy; tumour; cancer.

Homo sapiens.

US2003013855-A1.

16-JAN-2003.

03-MAY-2002; 2002US-0063616.

30-DEC-1998; 98KR-0062142.  
08-MAR-1999; 99WO-US05028.  
14-MAY-1999; 99WO-US10713.  
30-DEC-1999; 99WO-US1273.  
18-FEB-2000; 2000WO-US04341.  
01-MAR-2000; 2000WO-US05601.  
02-MAR-2000; 2000WO-US05841.  
21-MAR-2000; 2000WO-US07532.  
22-MAY-2000; 2000WO-US14042.  
02-JUN-2000; 2000WO-US15264.  
24-AUG-2000; 2000WO-US23328.  
10-NOV-2000; 2000WO-US30873.  
01-DEC-2000; 2000WO-US32678.  
20-DEC-2000; 2000WO-US34956.  
28-FEB-2001; 2001WO-US06520.  
01-JUN-2001; 2001WO-US17800.  
14-MAY-1999; 99US-0311832.  
25-AUG-1999; 99US-0380137.  
25-AUG-1999; 99US-0380138.  
25-AUG-1999; 99US-0380139.

25-AUG-1999; 99US-0380142.  
15-SEP-1999; 99US-0397342.  
18-OCT-1999; 99US-0403297.  
12-NOV-1999; 99US-0423844.  
22-AUG-2000; 2000US-0644848.  
18-SEP-2000; 2000US-0664610.  
18-SEP-2000; 2000US-0665350.  
08-NOV-2000; 2000US-0709238.  
20-DEC-2000; 2000US-0747259.  
22-MAR-2001; 2001US-0816744.  
10-MAY-2001; 2001US-0854208.  
10-MAY-2001; 2001US-0854280.  
30-MAY-2001; 2001US-0870574.  
03-JUN-2001; 2001US-0874503.  
28-JUN-2001; 2001US-0869599.  
18-JUL-2001; 2001US-0908827.  
06-DEC-2001; 2001US-0006867.  
(GETH ) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-330485/31.

N-PSDB; ACA58822.

New isolated antibody specifically binding a PRO polypeptide, useful  
for the preparation of a medicament for treating disorders with the  
aberrant expression or activity of the PRO polypeptide, such as tumor  
conditions and cancer -

Disclosure; Page 93; 406pp; English.

The invention relates to an antibody that binds to a polypeptide with a  
fully defined sequence given in the specification. The methods and  
compositions (containing antibodies that specifically bind a PRO  
polypeptide) of the present invention are useful for the preparation of a  
medicament for the treatment of disorders associated with the aberrant  
expression or activity of the PRO polypeptide, such as tumour conditions  
and cancer. They can also be used to generate transgenic or knockout  
animals useful in the development and screening of therapeutically useful  
reagents. The PRO polypeptides and encoding nucleic acids can be used as  
molecular weight markers for protein electrophoresis, chromosome  
identification and tissue typing. The PRO polypeptides are useful to  
induce angiogenesis e.g wound healing; in the treatment of sports-related  
joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The  
antibodies may be used in various diagnostic, competitive binding and/or  
immunoprecipitation assays. The present sequence represents the amino  
acid sequence of a PRO polypeptide of the invention.

SQ Sequence 119 AA;

Query Match 100.0%; Score 644; DB 24; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRMLQEGGQCECKDWFLRAP 60  
DB 1 MKYLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRMLQEGGQCECKDWFLRAP 60  
QY 61 RRKFMVTYSGLPKKQPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119  
DB 61 RRKFMVTYSGLPKKQPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119

RESULT 13

ABU71964

ID ABU71964 standard; Protein; 119 AA.

XX ABU71964;

XX 11-JUN-2003 (first entry)  
DT

## Novel human secreted and transmembrane protein PRO842.

Human; secreted and transmembrane polypeptide;  
chromosome mapping; gene mapping; transgenic animal; knockout animal;  
therapeutic agent screening; chromosome identification; tissue typing;  
gene therapy.

Homo sapiens.

US2003018183-A1.

23-JAN-2003.

01-MAY-2002; 2002US-0063512.

06-DEC-2001; 2001US-0006867.

(GETH ) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI: 2003-330984/31.

N-PSDB; ACA60375.

New secreted and transmembrane PRO polypeptides and nucleic acid  
molecules encoding the polypeptides, useful in gene therapy or  
preparing a medicament for treating a condition that is responsive to  
the PRO polypeptide or antibody.

Disclosure; Fig 26; 409pp; English.

The invention describes novel isolated PRO polypeptides. The PRO  
polypeptides or anti-PRO antibodies are useful in preparing a medicament  
for treating a condition that is responsive to the PRO polypeptide or  
antibody. The PRO nucleotide sequences may be used as hybridisation  
probes in chromosome and gene mapping, or in generating antisense RNA  
and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,  
in assays to identify other proteins or molecules involved in binding  
reaction, to generate transgenic animals or knockout animals, which in  
turn are useful in the development and screening of therapeutically  
useful reagents, for chromosome identification, and tissue typing. The  
PRO polypeptides and nucleic acid molecules are also useful in gene  
therapy, and as molecular weight markers for protein electrophoresis  
purposes. The anti-PRO antibodies may be used in diagnostic assays for  
PRO, or for the affinity purification of PRO from recombinant cell  
culture or natural sources. This is the amino acid sequence of a novel  
human secreted and transmembrane PRO polypeptide.

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 24; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

b 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

Y 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQQLKQCLRSFALPL 119

b 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQQLKQCLRSFALPL 119

## RESULT 14

BU72121

D ABU72121 standard; Protein; 119 AA.

X C ABU72121;

X T 13-JUN-2003 (first entry)

X X

Human PRO polypeptide #13.

Human; PRO polypeptide; secreted and transmembrane protein;  
anti-PRO antibody; diagnostic assay; gene expression.

Homo sapiens.

US2003023042-A1.

30-JAN-2003.

01-MAY-2002; 2002US-0063502.

06-DEC-2001; 2001US-0006867.

(GETH ) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI: 2003-331484/31.

N-PSDB; ACA63385.

Novel monoclonal antibody that binds to secreted and transmembrane  
polypeptide, useful for detecting and purifying the polypeptide and  
also for treating conditions responsive to the antibody.

Disclosure; Fig 26; 408pp; English.

The present invention relates to the isolation of novel human PRO  
polypeptides, and the polynucleotide sequences encoding them. The  
PRO polypeptides are secreted and transmembrane proteins. The PRO  
polypeptides and polynucleotides are useful for preparing a  
medicament useful in the treatment of a condition responsive to  
anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic  
assays for PRO, by detecting its expression in specific cells,  
tissues or serum, and for affinity purification of PRO from  
recombinant cell culture or natural sources. ABU72109-ABU72192  
represent the human PRO polypeptides of the invention.

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 24; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-66;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

QY 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQQLKQCLRSFALPL 119

Db 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQQLKQCLRSFALPL 119

## RESULT 15

ABU65638

ID ABU65638 standard; Protein; 119 AA.

X C ABU65638;

X X 19-MAY-2003 (first entry)

X X Human secreted/transmembrane protein, SEQ ID 140.

Human; PRO; secreted protein; transmembrane protein;  
cystostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;  
colon tumour; breast tumour; prostate tumour; rectal tumour;  
cervical tumour; liver tumour; TNF-alpha release; arthritis;  
tumour necrosis factor alpha; chondrocyte cell; bone disorder;  
cartilage disorder; sports injury.

Homo sapiens.

OS

US2003036156-A1.  
20-FEB-2003.

02-JUL-2002; 2002US-0188767.

16-SEP-1998; 98WO-US19330.  
07-OCT-1998; 98WO-US21141.  
01-DEC-1998; 98WO-US21108.  
08-MAR-1999; 99WO-US05028.  
14-MAY-1999; 99WO-US10733.  
02-JUN-1999; 99WO-US12252.  
01-SEP-1999; 99WO-US20111.  
15-SEP-1999; 99WO-US21090.  
01-DEC-1999; 99WO-US28301.  
02-DEC-1999; 99WO-US28551.  
30-DEC-1999; 99WO-US31274.  
08-JAN-2000; 2000WO-US00219.  
18-FEB-2000; 2000WO-US04341.  
18-FEB-2000; 2000WO-US04342.  
22-FEB-2000; 2000WO-US04414.  
24-FEB-2000; 2000WO-US05004.  
01-MAR-2000; 2000WO-US05601.  
02-MAR-2000; 2000WO-US05841.  
15-MAR-2000; 2000WO-US06884.  
30-MAR-2000; 2000WO-US08439.  
17-MAY-2000; 2000WO-US13705.  
22-MAY-2000; 2000WO-US14042.  
30-MAY-2000; 2000WO-US14941.  
02-JUN-2000; 2000WO-US15264.  
28-JUL-2000; 2000WO-US20710.  
24-AUG-2000; 2000WO-US23328.  
08-NOV-2000; 2000WO-US30352.  
01-DEC-2000; 2000WO-US32678.  
20-DEC-2000; 2000WO-US34956.  
28-FEB-2001; 2001WO-US06520.  
01-JUN-2001; 2001WO-US17800.  
20-JUN-2001; 2001WO-US19692.  
29-JUN-2001; 2001WO-US21066.  
09-JUL-2001; 2001WO-US21735.  
29-AUG-2001; 2001WO-US27099.  
18-SEP-1997; 97US-059283P.  
18-SEP-1997; 97US-059286P.  
17-OCT-1997; 97US-062250P.  
21-OCT-1997; 97US-063486P.  
24-OCT-1997; 97US-063120P.  
24-OCT-1997; 97US-063121P.  
28-OCT-1997; 97US-063540P.  
28-OCT-1997; 97US-063541P.  
28-OCT-1997; 97US-063544P.  
28-OCT-1997; 97US-063564P.  
29-OCT-1997; 97US-063734P.  
31-OCT-1997; 97US-063870P.  
31-OCT-1997; 97US-064103P.  
31-OCT-1997; 97US-065311P.  
13-NOV-1997; 97US-065117P.  
21-NOV-1997; 97US-066120P.  
24-NOV-1997; 97US-066466P.  
24-NOV-1997; 97US-066772P.  
11-DEC-1997; 97US-069335P.  
12-DEC-1997; 97US-069425P.  
17-DEC-1997; 97US-069870P.  
18-DEC-1997; 97US-068017P.  
10-MAR-1998; 98US-077450P.  
11-MAR-1998; 98US-077632P.  
11-MAR-1998; 98US-077649P.  
20-MAR-1998; 98US-078866P.  
20-MAR-1998; 98US-078939P.  
27-MAR-1998; 98US-079564P.  
27-MAR-1998; 98US-079786P.  
31-MAR-1998; 98US-080107P.  
31-MAR-1998; 98US-080194P.  
01-APR-1998; 98US-080327P.

01-APR-1998; 98US-080333P.  
08-APR-1998; 98US-081049P.  
08-APR-1998; 98US-081070P.  
09-APR-1998; 98US-081195P.  
13-APR-1998; 98US-081838P.  
21-APR-1998; 98US-082568P.  
21-APR-1998; 98US-082569P.  
22-APR-1998; 98US-082704P.  
22-APR-1998; 98US-082797P.  
28-APR-1998; 98US-083322P.  
29-APR-1998; 98US-083495P.  
29-APR-1998; 98US-083496P.  
29-APR-1998; 98US-083499P.  
29-APR-1998; 98US-083559P.  
03-MAY-1998; 98US-084366P.  
06-MAY-1998; 98US-084414P.  
07-MAY-1998; 98US-084639P.  
07-MAY-1998; 98US-084640P.  
07-MAY-1998; 98US-084643P.  
15-MAY-1998; 98US-085579P.  
15-MAY-1998; 98US-085580P.  
15-MAY-1998; 98US-085582P.  
15-MAY-1998; 98US-085700P.  
18-MAY-1998; 98US-086023P.  
22-MAY-1998; 98US-086392P.  
22-MAY-1998; 98US-086486P.  
28-MAY-1998; 98US-087098P.  
28-MAY-1998; 98US-087208P.  
02-JUN-1998; 98US-087609P.  
02-JUN-1998; 98US-087759P.  
04-JUN-1998; 98US-088025P.  
04-JUN-1998; 98US-088028P.  
04-JUN-1998; 98US-088029P.  
04-JUN-1998; 98US-088033P.  
04-JUN-1998; 98US-088326P.  
04-JUN-1998; 98US-088616P.  
05-JUN-1998; 98US-088202P.  
05-JUN-1998; 98US-088212P.  
09-JUN-1998; 98US-088217P.  
09-JUN-1998; 98US-088655P.  
10-JUN-1998; 98US-088722P.  
10-JUN-1998; 98US-088738P.  
10-JUN-1998; 98US-088740P.  
10-JUN-1998; 98US-088811P.  
10-JUN-1998; 98US-088824P.  
10-JUN-1998; 98US-088825P.  
10-JUN-1998; 98US-088826P.  
11-JUN-1998; 98US-088861P.  
11-JUN-1998; 98US-088863P.  
11-JUN-1998; 98US-088876P.  
11-JUN-1998; 98US-089090P.  
12-JUN-1998; 98US-089105P.  
16-JUN-1998; 98US-089512P.  
16-JUN-1998; 98US-089514P.  
17-JUN-1998; 98US-089538P.  
17-JUN-1998; 98US-089598P.  
17-JUN-1998; 98US-089653P.  
18-JUN-1998; 98US-089908P.  
19-JUN-1998; 98US-089952P.  
22-JUN-1998; 98US-090246P.  
22-JUN-1998; 98US-090252P.  
22-JUN-1998; 98US-090254P.  
24-JUN-1998; 98US-090439P.  
24-JUN-1998; 98US-090435P.  
24-JUN-1998; 98US-090444P.  
24-JUN-1998; 98US-090461P.  
24-JUN-1998; 98US-090535P.  
24-JUN-1998; 98US-090540P.  
25-JUN-1998; 98US-090676P.  
25-JUN-1998; 98US-090678P.  
25-JUN-1998; 98US-090688P.  
25-JUN-1998; 98US-090690P.

Query Match	Best Local Similarity	100.0%; Score 644; DB 24; Length 119;	0;	0;
Matches 119; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
25-JUN-1998;	98US-090694P.			
25-JUN-1998;	98US-090695P.			
25-JUN-1998;	98US-090696P.			
26-JUN-1998;	98US-090862P.			
26-JUN-1998;	98US-090863P.			
26-JUN-1998;	98US-091010P.			
01-JUL-1998;	98US-091359P.			
01-JUL-1998;	98US-091544P.			
02-JUL-1998;	98US-091478P.			
02-JUL-1998;	98US-091486P.			
02-JUL-1998;	98US-091628P.			
02-JUL-1998;	98US-091628P.			
02-JUL-1998;	98US-091632P.			
24-JUL-1998;	98US-094006P.			
04-AUG-1998;	98US-095282P.			
10-AUG-1998;	98US-095998P.			
10-AUG-1998;	98US-096012P.			
17-AUG-1998;	98US-096757P.			
17-AUG-1998;	98US-096766P.			
17-AUG-1998;	98US-096867P.			
17-AUG-1998;	98US-096891P.			
17-AUG-1998;	98US-096897P.			
18-AUG-1998;	98US-096949P.			
18-AUG-1998;	98US-096959P.			
18-AUG-1998;	98US-097022P.			
26-AUG-1998;	98US-097952P.			
26-AUG-1998;	98US-097954P.			
26-AUG-1998;	98US-097955P.			
26-AUG-1998;	98US-097971P.			
26-AUG-1998;	98US-097974P.			
26-AUG-1998;	98US-098014P.			
01-SEP-1998;	98US-098716P.			
01-SEP-1998;	98US-098723P.			
02-SEP-1998;	98US-098803P.			
02-SEP-1998;	98US-098821P.			
02-SEP-1998;	98US-098843P.			
09-SEP-1998;	98US-099602P.			
10-SEP-1998;	98US-099741P.			
1 MKVLISSLLLLPLMLMSVSSLLPNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60				
1 MKVLISSLLLLPLMLMSVSSLLPNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60				
61 RRKFMTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRAQQQLKQCLRSFALPL 119				
61 PRKFMVSYGPRKQPCDHFKNVKKTRHQRHHRKPNKHSRAQQQLKQCLRSFALPL 119				

arch completed: September 13, 2003, 14:43:47  
b time : 55.6667 secs

sult No.	Score	Query		Length	DB	ID	Description
		Match					
1	77.5	12.0	477	2	TJ18801		hypothetical prote
2	77	12.0	2269	1	QJ1750		genome polyprotein
3	74.5	11.6	448	2	A50451		vitamin D receptor
4	73.5	11.4	70	2	A60912		vitamin D receptor
5	71.5	11.1	108	2	G84522		similar to gibbere
6	71	11.0	411	2	S35333		steroid receptor p
7	71	11.0	2262	2	S16564		large protein L -
8	71	11.0	3190	2	T13828		CREB-binding prote
9	70.5	10.9	1283	2	T49804		hypothetical prote
10	70	10.9	543	2	A32693		steroid receptor p
11	70	10.9	746	2	B32693		steroid receptor p
12	70	10.9	1095	2	T24061		hypothetical prote
13	70	10.9	1620	2	T27283		hypothetical prote
14	69.5	10.8	221	2	C37468		ORF2 protein - Orf
15	69.5	10.8	575	1	TH4013		thrombomodulin pre
16	69	10.7	200	2	C83986		hypothetical prote
17	68.5	10.6	381	2	A46358		steroid/thyroid ho
18	68.5	10.6	422	2	PC4019		vitamin D receptor
19	68.5	10.6	423	2	A31761		1,25-dihydroxyvita
20	68.5	10.6	427	2	A28200		vitamin D receptor
21	68.5	10.6	427	2	S24174		vitamin D receptor
22	68.5	10.6	647	2	S36557		E1 protein - human
23	68.5	10.6	1006	2	S74992		hypothetical prote
24	68	10.6	283	2	S42393		G-box-binding prot
25	67	10.4	376	2	T48350		cysteine proteinas
26	67	10.4	475	2	B69843		histidine permease
27	67	10.4	1062	2	T14151		Inv protein - mous
28	67	10.4	1062	2	T30355		inversin - mouse
29	66.5	10.3	103	2	A72713		hypothetical prote

F;1-70/Domain: erBA transforming protein homology (fragment) <ERBA>

Query Match 11.4%; Score 73.5; DB 2; Length 70;  
Best Local Similarity 35.5%; Pred. No. 1.1;  
Matches 22; Conservative 9; Mismatches 12; Indels 19; Gaps 5;

QY 50 CE-CXDFLRAPRRKMTVSGLPKQCPCDHFCKGNVKTRHORHHRKPKNHSRACQOFLK 108  
|||:::||:||||||| | |||:::||:  
Db 20 CEGCKGFFRRSMKRKAMFT-----CP---FNGDKITKDNR-----RHQQACR--LK 61

QY 109 QC 110  
||  
Db 62 RC 63

RESULT 5

G84522  
similar to giberellin-regulated proteins [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 01-Mar-2002  
C;Accession: G84522  
R.;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; UID:20083487; PMID:10617197  
A;Accession: G84522  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-108 <STO>  
A;Cross-references: GB:AE002093; NID:g3650032; PIDN:AAC61287.1; GSFD:GN00139  
C;Genetics:  
A;Gene: At2g14900  
A;Map position: 2  
C;Superfamily: gibberellin-regulated protein GAS42

Query Match 11.1%; Score 71.5; DB 2; Length 108;  
Best Local Similarity 25.9%; Pred. No. 2.7;  
Matches 29; Conservative 18; Mismatches 38; Indels 27; Gaps 7;

QY 1 MKVLSSLLLL-LPLMLMSVSSSLNPGVARG-----HRDRGQAQRRLQLGGQECE-- 51  
|||:::||:||||||| | |||:::||:  
Db 1 MKTIIVSILVLASLLLSSLSATISDAFGSGAVAFAPQSKDGPALEKWCV--GQKCEGR 57

QY 52 CXDWFLRAPRRKMTVSGLPKQCPCDHFCKGNVKTRHORHHRKPKNHSRAC 103  
|||:::||:||||||| | |||:::||:  
Db 58 CKP---AGMKRDOLKYCGICKDCQC-----VPSCGY-----GNKHBCAC 94

RESULT 6

S35333  
steroid receptor protein svp44 - zebra fish  
C;Species: Brachydanio rerio (zebra fish)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 24-Sep-1999  
C;Accession: S35333  
R.Fjose, A.; Nornes, S.; Weber, U.; Mlodzik, M.  
EMBO J. 12, 1403-1414, 1993  
A;Title: Functional conservation of vertebrate seven-up related genes in neurogenesis  
A;Reference number: S35333; UID:93223680; PMID:8467797  
A;Accession: S35333  
A:Molecule type: mRNA  
A;Residues: 1-411 <EJO>  
A;Cross-references: EMBL:X70299; NID:g296418; PIDN:CAA49780.1; PID:g296419  
C;Genetics:  
A;Gene: svp44  
C;Superfamily: unassigned erba-related proteins; erBA transforming protein homology  
C;Keywords: DNA binding; steroid hormone receptor; zinc finger  
F;74-320/Domain: erBA transforming protein homology <ERBA>  
F;75-96/Region: zinc finger  
F;112-136/Region: zinc finger

Query Match 11.0%; Score 71; DB 2; Length 411;

Dd 2430 QHTKNCK--RKPNNGCPICKQLIALC 2453

RESULT 9  
T49804  
hypothetical protein BllB22.60 [imported] - Neurospora crassa  
C:Species: Neurospora crassa  
C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T49804  
R:Schulte, U.; Align, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakutu  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: Z25022  
A:Accession: T49804  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1283 <SCH>  
A:Cross-references: EMBL:AL356834; GSPDB:GNO0116; NCSP:BllB22.60  
A:Experimental source: BAC clone BllB22; strain OR74A  
C:Genetics:  
A:Gene: NCSP:BllB22.60  
A:Map position: 6  
A:Introns: 856/2

Query Match 10.9%; Score 70.5; DB 2; Length 1283;  
Best Local Similarity 24.5%; Pred. No. 29;  
Matches 26; Conservative 18; Mismatches 31; Indels 31; Gaps 6;

QY 33 RDQGASRRWLQEGGECECKDWFLRAPRKFTVVS---GLPKKQCPCDHFGKNVK--T 87  
||| :||| : ||| | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db 454 RNKMKKQKWKEGSGSK-----LRAPESAMPVPVVMGSPSRAWPLRWOGHIRNGDV 508  
||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 88 RHQRHHR-----KPNKHSRACQF--LKOCQLRSFA 116  
||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db 509 GHSHNHQMYMDGYVRWLSEKLEPH----QQFARLRKAELALYA 550  
||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 10  
A32693  
steroid receptor protein svp 1 - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 20-Sep-1999  
C:Accession: A32693  
R:Modzik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.  
Cell 60, 211-224, 1990  
A:Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfamily  
A:Reference number: A32693; MUID:90124631; PMID:2105166  
A:Accession: A32693  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-543 <MLO>  
A:Cross-references: GB:M28963; NID:g158518; PIDN:AAA62770.1; PID:g158519.  
C:Genetics:  
A:Gene: FlyBase:svp  
A:Cross-references: FlyBase:FBgn0003651  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription  
E:198-452/Domain: erba transforming protein homology <ERBA>  
E:200-220/Region: zinc finger  
E:236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 543;  
Best Local Similarity 26.7%; Pred. No. 16;  
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

QY 21 SSSLNPG-----VARGHDRGASRRWLQEGGECECKDWFLRAPRKFTVSG 69  
||| | ||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db 183 SQSNSSGSQDSKONIECVCGDKSSKHVGQTCEG-----CKSFPRSVRRN-LIYSC 236  
||| | ||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 70 LPKKQCCPDHFKNVKKTRHQRRHKRPKNHSRACQQLKOC 110  
||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db 237 RGRNRCPTD-----QHNRNQCYCR-----LKKC 260  
||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :



## SULT 11

2693  
eroid receptor protein svp 2 - fruit fly (Drosophila melanogaster)  
Species: Drosophila melanogaster  
Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 12-Sep-1997  
Accession: B32693  
Miodzik, M.; Hironi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.  
11 60, 211-224, 1990  
Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfamily  
Reference number: A36693; MUID:90124631; PMID:2105166  
Accession: B32693  
Status: preliminary  
Molecule type: mRNA  
Residues: 1-746 <MLO>  
Cross-references: GB:M28863; GB:M28864  
Genetics:  
Gene: FlyBase:svp  
Cross-references: FlyBase:FBgn0003651  
Superfamily: unassigned erba-related proteins; erba transforming protein homology  
Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription  
198-452/Domain: erba transforming protein homology <ERBA>  
200-220/Region: zinc finger  
236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 746;  
Best Local Similarity 26.7%; Pred. No. 21;  
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;  
21 SSSINPG-----VARGHRRGQASRRWLQGGQCECKDWFLRAPRRKFMVSG 69  
183 SQSSNSGSDSKQNTIECVCGDKSGRHVGFCEG-----CKSFFKRSVRRN-LIYSC 236  
70 LPKQPCPDHFGKGNVKKTRHQRHRRKPNKHSRACQFLKQC 110  
237 RGRNCPID-----QHRNQCOYCR-----LKKC 260

## SULT 12

4061  
pothetical protein R09A8.1 - Caenorhabditis elegans  
Species: Caenorhabditis elegans  
Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
Accession: T24061  
Wilkinson, J.  
mitted to the EMBL Data Library, November 1995  
Reference number: Z19836  
Accession: T24061  
Status: preliminary; translated from GB/EMBL/DDBJ  
Molecule type: DNA  
Residues: 1-1095 <WIL>  
Cross-references: EMBL:Z68009; PIDN:CAA92003.1; GSPDB:GN00028; CESP:R09A8.1  
Experimental source: clone R09A8  
Genetics:  
Gene: CESP:R09A8.1  
Map position: X  
Introns: 48/2; 189/1; 285/3; 347/3; 402/3; 482/3; 543/3; 619/1; 693/1; 771/1; 835/1; 1

Query Match 10.9%; Score 70; DB 2; Length 1095;  
Best Local Similarity 31.6%; Pred. No. 29;  
Matches 24; Conservative 10; Mismatches 32; Indels 10; Gaps 3;  
20 VSSSLNPGVARGHRRGQASRRWLQGGQCECKDWFLRAPRRKFMVSGLPKQPCDH 79  
305 VQSSLMYGGNRSTDYRNA-ORFASTGFVEKECRWDQLVERKQ-----KKEVNSDH 355  
80 FKGNVKKTRHQRHRRK 95  
356 KKAN-RITSLHNSR 370

## SULT 13

7283  
pothetical protein Y64G10A.f - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T27283  
R:Ainscough, R.  
submitted to the EMBL Data Library, September 1999  
A:Reference number: Z20336  
A:Accession: T27283  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1620 <WIL>  
A:Cross-references: EMBL:AL110498; NID:el542303; PIDN:CAB54471.1; CESP:Y64G10A.f  
A:Experimental source: clone Y64G10A  
C:Genetics:  
A:Gene: CESP:Y64G10A.f  
A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1

Query Match 10.9%; Score 70; DB 2; Length 1620;  
Best Local Similarity 30.0%; Pred. No. 40;  
Matches 21; Conservative 10; Mismatches 35; Indels 4; Gaps 3;  
QY 46 GGQCECKDWF-LRAPRRKFMVSGLPKQPCDHFGKGNVKKTRH--QRHRRKPNKHSRA 102  
Db 261 GRAQCOQYPCFHLSDRRSCVDIDECANN-GCEHFCENVKTYRCKREGYQLGRDGT 319  
QY 103 COQFLKQCQL 112  
Db 320 CEEMUGGCQV 329

## RESULT 14

C34768  
ORF2 protein - Orf virus (strain NZ2)  
C:Species: Orf virus  
C:Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 08-Oct-1999  
C:Accession: C34768  
R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.  
Virology 176, 379-389, 1990  
A:Title: Sequence analysis of the inverted terminal repetition in the genome of the p  
A:Reference number: A34768; MUID:90266454; PMID:2129563  
A:Accession: C34768  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-221 <FRA>  
A:Cross-references: GB:M30023; EMBL:M37623; NID:g332561; PIDN:AAA46789.1; PID:g332565

Query Match 10.8%; Score 69.5; DB 2; Length 221;  
Best Local Similarity 29.2%; Pred. No. 8.1;  
Matches 33; Conservative 8; Mismatches 37; Indels 35; Gaps 6;  
QY 26 PGVARGHRRGQASRRWLQGGQCECKDWFLRAPRRKFMVSGLPK-----QCP 76  
Db 83 PAAARGARRRGCCARRARGGWP---RWRPRAARRG---SGPPARAPAAALAPDQAP 135  
QY 77 CDHFGKGNVKKTR-----HQR--HHRKPNKHSRACQFLKQCQLRS 114  
Db 136 ----RSKVKDLRAVETLPQPTHTLPPARROHRSQQAQCTPRRAGCSARS 184

## RESULT 15

THUB  
thrombomodulin precursor [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1988 #sequence\_revision 12-May-1995 #text\_change 15-Sep-2000  
R:Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruy  
J. Biochem. 103, 281-285, 1988  
A:Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed ac  
A:Reference number: A41442; MUID:88227901; PMID:2836377  
A:Accession: A41442  
A:Molecule type: DNA  
A:Residues: 1-575 <SHI>  
A:Cross-references: DDBJ:D00210; NID:g220126; PIDN:BAA00149.1; PID:g220127  
R:Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.

roc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987  
 Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN  
 Reference number: A28307; MUID:87317665; PMID:2819876  
 Accession: A28307  
 Molecule type: DNA; mRNA  
 Residues: 1-472, 'A', 474-575 <JAC>  
 Cross-references: GB:J02973; NID:G339658; PIDN:AAA61175.1; PID:G339659  
 Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishio, J.; Maruyama, I.; Zushi, M.; Kawaha  
 40 J. 6, 1891-1897, 1987  
 Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth  
 Reference number: A29680; MUID:88004395; PMID:2820710  
 Accession: A29680  
 Molecule type: mRNA  
 Residues: 1-575 <SUZ>  
 Cross-references: GB:X05495; NID:G37123; PIDN:CAA29045.1; PID:G736251  
 Experimental source: lung endothelium  
 Note: part of this sequence, including the amino end of the mature protein, were deter  
 Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.  
 ochemistry 26, 4350-4357, 1987  
 Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the  
 Reference number: A27073; MUID:88024950; PMID:2822087  
 Accession: A27073  
 Molecule type: mRNA  
 Residues: 1-472, 'A', 474-575 <WEN>  
 Cross-references: GB:M16552; NID:G339656; PIDN:AAB59508.1; PID:G339657  
 Experimental source: placenta  
 Note: parts of this sequence were determined by protein sequencing  
 Yamamoto, S.; Mizouchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.  
 Biochem 113, 433-440, 1993  
 Title: Urinary thrombomodulin, its isolation and characterization.  
 Reference number: JX0264; MUID:93293792; PMID:8390446  
 Accession: JX0264  
 Molecule type: protein; mRNA  
 Residues: 19-472, 'A', 474-486 <YAM>  
 Experimental source: urine  
 Note: the urinary form appears to be identical with that circulating in plasma  
 Gerlitz, B.; Hassell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.  
 ochem. J. 295, 131-140, 1993  
 Title: Identification of the predominant glycosaminoglycan-attachment site in soluble  
 protein.  
 Reference number: S38954; MUID:94029900; PMID:8216207  
 Accession: S38954  
 Molecule type: protein  
 Residues: 475-491, 'X', 493-494 <GER>  
 Note: the residue designated 'X' was determined to be a Ser with covalently bound chor  
 Meininger, D.P.; Komives, E.A.  
 Submitted to the Brookhaven Protein Data Bank, September 1995  
 Reference number: A57369; PDB:1ZAQ  
 Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue  
 Tulinsky, A.; Mathews, I.I.  
 Submitted to the Brookhaven Protein Data Bank, August 1994  
 Reference number: A52804; PDB:1HLT  
 Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442  
 Hrabal, R.; Komives, E.A.; Ni, F.  
 Submitted to the Brookhaven Protein Data Bank, November 1995  
 Reference number: A65583; PDB:1FGD  
 Contents: annotation; conformation by (1)H-NMR, residues 427-444  
 Hrabal, R.; Komives, E.A.; Ni, F.  
 otein Sci. 5, 195-203, 1996  
 Title: Structural resiliency of an EGF-like subdomain bound to its target protein, the  
 Reference number: A58595; MUID:96276211; PMID:8745396  
 Contents: annotation; conformation by (1)H-NMR  
 Genetics:  
 Gene: GDB:THBD  
 Cross-references: GDB:119613; OMIM:188040  
 Map position: 20p11.2-20p11.2  
 Introns: #status absent  
 Complex: homodimer, urinary form  
 Function:  
 Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat  
 Pathway: blood coagulation moderation  
 Note: the membrane-bound form is located on the endothelium luminal surface of arterie  
 Note: thrombin complexed with the membrane-bound form is subject to endocytosis

C/Superfamily: thrombomodulin; C-type lectin homology; EGF homology  
 C/Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood c  
 e protein  
 F.1-18/Domain: signal sequence #status predicted <SIG>  
 F.19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>  
 F.19-513/Domain: extracellular #status predicted <EXT>  
 F.19-486/Product: thrombomodulin, urinary form #status experimental <MAU>  
 F.24-167/Domain: C-type lectin homology <LCH>  
 F.177-199/Region: PEST sequence  
 F.201-233/Region: PEST sequence  
 F.245-280/Domain: EGF homology <EG1>  
 F.288-323/Domain: EGF homology <EG2>  
 F.328-362/Domain: EGF homology <EG3>  
 F.363-404/Domain: EGF homology <EG4>  
 F.408-439/Domain: EGF homology <EG5>  
 F.445-480/Domain: EGF homology <EG6>  
 F.485-513/Region: PEST sequence  
 F.517-539/Domain: transmembrane #status predicted <TMN>  
 F.540-575/Domain: intracellular #status predicted <INT>  
 F.47,115,116,382,409/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F.174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F.245-256,252-265,267-280,288-296,292-308,310-323,329-340,336-349,351-362,369-378,374  
 F.334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F.342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental  
 F.490,492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experi  
 Query Match 10.88; Score 69.5; DB 1; Length 575;  
 Best Local Similarity 23.58; Pred. No. 18; Mismatches 26; Indels 41; Gaps 5;  
 Matches 24; Conservative 11;  
 QY 5 ISSLLLLPLMLMSVSSSLNPGVARGHRDGRGARRW---LQEGQECECKDFLRAPP 61  
 Db 209 VGSSAAVAPLGLQLMCTAP--PGAVQGHWR-EAPGAWDCSVENGSCHEACN----- 257  
 QY 62 RKFTVSGLPKKQCP-----CDHF 80  
 Db 258 ----AIPGAPRCQCPAGALQADGRCTASATOSCNLDCEHF 295  
 Search completed: September 13, 2003, 14:50:26  
 Job time : 21.6667 secs

GenCore version 5.1.6  
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4 protein - protein search, using sw model

on: September 13, 2003, 14:32:52 ; Search time 11.3333 Seconds  
 (without alignments)  
 493.780 Million cell updates/sec

tle: US-09-786-260-1  
 arfect score: 644  
 equence: 1 MKVLISLLILLPLMLMSV.....SRACQFLKQQLRSFALPL 119

oring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

arched: 127863 seqs, 47026705 residues

tal number of hits satisfying chosen parameters: 127863

inimum DB seq length: 0  
 aximum DB seq length: 2000000000

st-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

atabase : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	77	12.0	2269	1	RRPL_SV41
2	74.5	11.6	448	1	VDR_COA1
3	74.5	11.6	451	1	VDR_CHICK
4	72.5	11.3	3313	1	CUR3_RAT
5	71	11.0	411	1	SV44_BRARE
6	71	11.0	1798	1	LMB2_HUMAN
7	71	11.0	2262	1	RRPL_P12HT
8	70	10.9	543	1	7UP1_DROME
9	70	10.9	746	1	7UP2_DROME
10	69.5	10.8	575	1	TEBM_HUMAN
11	69	10.7	314	1	SIX3_CHICK
12	68.5	10.6	422	1	VDR_MOUSE
13	68.5	10.6	422	1	VDR_XENLA
14	68.5	10.6	423	1	VDR_RAT
15	68.5	10.6	424	1	VDR_BOVIN
16	68.5	10.6	427	1	VDR_HUMAN
17	68.5	10.6	647	1	VE1_HPAV0
18	67	10.4	376	1	CER2_ARATH
19	67	10.4	475	1	RTM_BACSU
20	67	10.4	529	1	YB98_HUMAN
21	66.5	10.3	422	1	COT1_MOUSE
22	66.5	10.3	423	1	COT1_HUMAN
23	66.5	10.3	424	1	COT1_BOVIN
24	66.5	10.3	3301	1	CLR3_MOUSE
25	66	10.2	1539	1	SNCY_HUMAN
26	65.5	10.2	646	1	VE1_HPV07
27	65.5	10.2	706	1	FZD6_HUMAN
28	65	10.1	363	1	PGL1_COLLN
29	65	10.1	441	1	COAT_SOCMY
30	64.5	10.0	534	1	2397_HUMAN
31	64.5	10.0	622	1	MAK_MOUSE
32	64	9.9	227	1	TN77_HUMAN
33	64	9.9	246	1	SIX6_CHICK

## ALIGNMENTS

## RESULT 1

RRPL\_SV41  
 ID RRPL\_SV41 STANDARD; PRT; 2269 AA.  
 AC P35341;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-2003 (Rel. 41, Last annotation update)  
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
 DE (L protein).  
 GN L.  
 OS Simian virus 41 (SV41).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
 OX NCBI\_TaxID=11228;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Toshiba/Chanock;  
 RX MEDLINE=93019033; PubMed=1328485;  
 RA Ogawa N., Mutsaers N., Tsurudome M., Kawano M., Matsumura H.,  
 RA Kusagawa S., Komada H., Nishio M., Ito Y.;  
 RT "Nucleotide sequence analysis of the simian virus 41 gene encoding  
 the large (L) protein and construction of a phylogenetic tree for the  
 L proteins of paramyxoviruses.";  
 RT J. Gen. Virol. 73:2743-2750(1992).  
 RL J. Gen. Virol. 73:2743-2750(1992).  
 CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY  
 CC FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)  
 CC SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAs, RNA EDITING OF THE P  
 CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.  
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC [RNA](N).  
 CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X64275; CAA45569.1;  
 CC PIR: JQ1750; JQ1750.  
 CC InterPro: IPR007098; RNA\_pol\_monon.  
 CC InterPro: IPR001016; Viral\_RNA\_pol.L.  
 CC Pfam: PF00946; Paramyx\_RNA\_pol; 1.  
 CC Transferrase; RNA-directed RNA polymerase.  
 CC KW Transferrase; RNA-directed RNA polymerase.  
 CC SEQUENCE 2269 AA; 256429 MW; 3BD60C14AA161F5B CRC64;

Query Match 12.0%; Score 77; DB 1; Length 2269;  
 Best Local Similarity 27.5%; Pred. No. 47; Gaps 6;  
 Matches 30; Conservative 12; Mismatches 31; Indels 36;  
 YQ 13 PLMLMSVSSSLNPGVARGHRDQGS-----RRWLQ-----EGQCEP--CK 53  
 DB 422 PLSLPGNASKSL-----TELHDNSEISYEYTLRWKLSLIEFKKCFDPPGELSIFMK 477

54 DWFLAPRRKEMTVSGLPKKQPCDHFKNVKKTRHORHH-RKPNKHSR 101  
 478 DKAISAPKEDWMSV-----FRSLIKQRHQRHHIPMPNPFNR 514

SULT 2

R\_COTJJA STANDARD; PRT; 448 AA.  
 P49701;  
 01-FEB-1996 (Rel. 33, Created)  
 01-FEB-1996 (Rel. 33, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).  
 VDR OR NR11.  
 Coturnix coturnix japonica (Japanese quail).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 Coturnix.  
 NCBI\_TaxID=93934;  
 [1]  
 SEQUENCE FROM N.A. (ISOFORMS A AND B).  
 TISSUE=Chorionicallantoic membrane;  
 MEDLINE=95062315; PubMed=7972109;  
 Etlaroussi M.A., Prah J.M., Deluca H.F.;  
 "The avian vitamin D receptors: primary structures and their  
 origins...";  
 Proc. Natl. Acad. Sci. U.S.A. 91:11596-11600(1994).  
 -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE  
 EXPRESSION OF HORMONE SENSITIVE GENES.  
 -!- SUBCELLULAR LOCATION: Nuclear.  
 -!- ALTERNATIVE PRODUCTS:  
 Event-Alternative initiation;  
 Comment=2 isoforms, A (shown here) and B, are produced by  
 alternative initiation;  
 -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI  
 subfamily.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL; U12641; AAA56725.1; -;  
 PIR; I50451; I50451.  
 HSSP; O75469; IILG.  
 InterPro; IPR000536; Hormone\_rec\_lig.  
 InterPro; IPR001723; Stdhrmn\_receptor.  
 InterPro; IPR001628; Znf\_C4steroid.  
 Pfam; PF00104; hormone\_rec; 1.  
 Pfam; PF00105; zf-C4; 1.  
 PRINTS; PR00398; STRDHORMONER.  
 PRINTS; PR00047; STROIDFINGER.  
 ProDom; PD000035; Znf\_C4steroid; 1.  
 SMART; SM00430; HOL1; 1.  
 SMART; SM00399; Znf\_C4; 1.  
 PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 Zinc-finger; Alternative initiation.  
 CHAIN 1 448 VITAMIN D3 RECEPTOR, ISOFORM A.  
 VITAMIN D3 RECEPTOR, ISOFORM B.  
 INIT\_MET 26 26 FOR ISOFORM B.  
 DNA\_BIND 44 109 NUCLEAR RECEPTOR-TYPE.  
 ZN\_FING 44 64 C4-TYPE.  
 ZN\_FING 80 104 C4-TYPE.  
 DOMAIN 110 212 HINGE.  
 DOMAIN 213 448 LIGAND-BINDING.  
 SEQUENCE 448 AA; 50668 MW; FCFIFC3DEAEAF3E CRC64;

Query Match 11.6%; Score 74.5; DB 1; Length 448;  
 Best Local Similarity 32.9%; Pred. No. 1.8;  
 Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;  
 QY 50 CE-CKDWFLAPRRKEMTVSGLPKKQPCDHFKNVKKTRHORHH-RKPNKHSRACQOFLK 108  
 DB 61 CEGCKGFFRRSRMKRAMFT-----CP---FSGDKITKDNR-----RHCQACR--LK 102  
 QY 109 QC-----QLRSFAL 117  
 DB 103 RCVDIGMKKEFIL 115  
 RESULT 3  
 VDR\_CHICK STANDARD; PRT; 451 AA.  
 ID VDR\_CHICK  
 AC O42392;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DT Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).  
 DE VDR OR NR11.  
 GN Gallus gallus (Chicken).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORMS A AND B).  
 RC STRAIN=Leghorn; TISSUE=Kidney;  
 RA MEDLINE=97223369; PubMed=9056239;  
 RA Lu Z., Hanson K., Deluca H.F.;  
 RT "Cloning and origin of the two forms of chicken vitamin D receptor.";  
 RL Arch. Biochem. Biophys. 339:99-106(1997).  
 [2]  
 RN SEQUENCE OF 45-114 FROM N.A.  
 RP MEDLINE=87149040; PubMed=3029866;  
 RA McDonnell D.P., Mangelsdorf D.J., Pike J.W., Haussler M.R.,  
 RA O'Malley B.W.;  
 RT "Molecular cloning of complementary DNA encoding the avian receptor  
 for vitamin D.";  
 RL Science 235:1214-1217(1987).  
 CC -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE  
 EXPRESSION OF HORMONE SENSITIVE GENES.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- ALTERNATIVE PRODUCTS:  
 Event-Alternative initiation;  
 Comment=2 isoforms, A (shown here) and B, are produced by  
 alternative initiation;  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.  
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI  
 subfamily.  
 -----  
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 -----  
 EMBL; AF011356; AAB62579.1; -;  
 PIR; A60912; A60912.  
 HSSP; O75469; IILG.  
 TRANSFAC; T00884; -;  
 InterPro; IPR000536; Hormone\_rec\_lig.  
 InterPro; IPR001723; Stdhrmn\_receptor.  
 InterPro; IPR001628; Znf\_C4steroid.  
 Pfam; PF00104; hormone\_rec; 1.  
 Pfam; PF00105; zf-C4; 1.  
 PRINTS; PR00398; STRDHORMONER.

```
PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger; Alternative initiation.
CHAIN 1 451 VITAMIN D3 RECEPTOR, ISOFORM A.
INIT_MET 15 451 VITAMIN D3 RECEPTOR, ISOFORM B.
NUCLEAR_BIND 47 112 FOR ISOFORM B.
NUCLEAR_RECEPTOR-TYPE.
ZN_FING 47 67 C4-TYPE.
ZN_FING 83 107 C4-TYPE.
DOMAIN 113 215 HINGE.
DOMAIN 216 451 LIGAND-BINDING.
SEQUENCE 451 AA; 51299 MW; 207986A6C8D8E5FC CRC64;

Query Match 11.6%; Score 74.5; DB 1; Length 451;
Best Local Similarity 32.9%; Pred. No. 1.8;
Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;

50 CE-CKDWFLAPRRKFWTVSGLPKQPCDHPKGNVKKTRHORHKKPKNSRACQQLK 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
64 CECKGFFRSMRKAMFT-----CP----FNGCKITKDN-----RHQACR--LK 105

109 QC-----QLRSFAL 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 RCVDIGMKKEFIL 118

SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-98360089; PubMed-9693030;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple
EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
-!- FUNCTION: Receptor that may have an important role in cell/cell
signaling during nervous system formation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in the brain. Expressed in
cerebellum, olfactory bulb, cerebral cortex, hippocampus and
brain stem.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: Contains 9 cadherin domains.
-!- SIMILARITY: Contains 8 EGF-like domains.
-!- SIMILARITY: Contains 2 laminin G-like domains.
-!- SIMILARITY: Contains 1 laminin EGF-like domain.
-!- SIMILARITY: Contains 1 GPS domain.

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or send an email to license@isb-sib.ch).
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EMBL; AB011528; BAA32459.1; -.
DR HSP; P00740; 1EDM.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm2_1.
DR Pfam; PF00028; cadherin; 9.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00205; CADHERIN.
DR PRINTS; PR00011; EGFLAMININ.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00112; CA; 9.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; HORM; 1.
DR SMART; SM0282; Lang; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00232; CADHERIN_1; 7.
DR PROSITE; PS00288; CADHERIN_2; 8.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS00221; GPS; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
KW Developmental protein; Signal; Hydroxylation; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 3313 CADHERIN EGF LAG SEVEN-PASS G-TYPE
RECEPTOR 3
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
CADHERIN 7.
CADHERIN 8.
CADHERIN 9.
EGF-LIKE 1. CALCIUM-BINDING.
EGF-LIKE 2. CALCIUM-BINDING.
EGF-LIKE 3. CALCIUM-BINDING.
LAMININ G-LIKE 1.
1710
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DOMAIN 1713 1749 EGF-LIKE 4, CALCIUM-BINDING.  
 DOMAIN 1753 1935 LAMININ G-LIKE 2.  
 DOMAIN 1937 1972 EGF-LIKE 5, CALCIUM-BINDING.  
 DOMAIN 1973 2011 EGF-LIKE 6, CALCIUM-BINDING.  
 DOMAIN 2012 2044 EGF-LIKE 7, CALCIUM-BINDING.  
 DOMAIN 2046 2081 EGF-LIKE 8, CALCIUM-BINDING.  
 DOMAIN 2087 2120 LAMININ EGF-LIKE.  
 DOMAIN 2120 2157 GPS.  
 DOMAIN 2157 2227 BY SIMILARITY.  
 DISULFID 1370 1381 BY SIMILARITY.  
 DISULFID 1375 1412 BY SIMILARITY.  
 DISULFID 1414 1423 BY SIMILARITY.  
 DISULFID 1430 1441 BY SIMILARITY.  
 DISULFID 1435 1450 BY SIMILARITY.  
 DISULFID 1452 1461 BY SIMILARITY.  
 DISULFID 1470 1481 BY SIMILARITY.  
 DISULFID 1475 1491 BY SIMILARITY.  
 DISULFID 1493 1504 BY SIMILARITY.  
 DISULFID 1717 1728 BY SIMILARITY.  
 DISULFID 1722 1737 BY SIMILARITY.  
 DISULFID 1739 1748 BY SIMILARITY.  
 DISULFID 1941 1952 BY SIMILARITY.  
 DISULFID 1946 1961 BY SIMILARITY.  
 DISULFID 1963 1972 BY SIMILARITY.  
 DISULFID 1976 1987 BY SIMILARITY.  
 DISULFID 1981 1999 BY SIMILARITY.  
 DISULFID 2001 2010 BY SIMILARITY.  
 DISULFID 2018 2031 BY SIMILARITY.  
 DISULFID 2033 2043 BY SIMILARITY.  
 DISULFID 2050 2065 BY SIMILARITY.  
 DISULFID 2052 2068 BY SIMILARITY.  
 DISULFID 2070 2080 BY SIMILARITY.  
 MOD\_RES 1954 1954 HYDROXYLATION (POTENTIAL).  
 CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 838 838 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 1173 1173 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 1213 1213 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 1308 1308 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 1318 1318 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 1640 1640 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 1704 1704 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 1761 1761 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 2044 2044 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 2173 2173 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 2192 2192 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 2382 2382 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 2472 2472 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 2504 2504 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SEQUENCE 3313 AA; 559348 MW; 511DA09517288764 CRC64;  
 Query Match 11.3%; Score 72.5; DB 1; Length 3313;  
 Best Local Similarity 27.6%; Pred. No. 20;  
 Matches 35; Conservative 9; Mismatches 40; Indels 43; Gaps 7;  
 24 LNPVGARGHRDGRQASRRWLEQ--GQCECKDWFL-----RAPRRKFTVSGLP 71  
 1978 LNP-----CQNGGCRHLQGGPHGTCDCAAGYFGQHCHEHMDQCCPRGHWGSGTGP 2030  
 72 KQCPDHPFGK---NVKTKRHRH-----HRKP-----NKHSRACQOFLKQC 110  
 2031 ---CNCVDHKGDPNCKNTSGQCHCKCFHYRPRGSDCLPCDYPVGSSTRSCAPHSGQC 2087  
 111 QLRSFAL 117  
 2088 PCRPGL 2094  
 SULT 5  
 44\_BRAE STANDARD; PRT; 411 AA.  
 SV44\_BRAE  
 Q06725;  
 15-JUL-1999 (Rel. 36, Created)  
 15-JUL-1999 (Rel. 38, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)

DE Steroid receptor homolog SVP 44.  
 GN SVP44 OR NR2F1.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93223680; PubMed=8467797;  
 RA Fjose A., Nornes S., Weber U., Mlodzik M.;  
 RT "Functional conservation of vertebrate seven-up related genes in  
 RT neurogenesis and eye development.";  
 RL EMBO J. 12:1403-1414(1993).  
 CC -1- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR  
 CC CELLS PRECURSORS DURING EYE DEVELOPMENT.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2  
 CC subfamily.  
 CC -----  
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 CC -----  
 DR EMBL; X70299; CAA49780.1; -;  
 DR PIR; S35333; S35333.  
 DR HSP; P19793; 2NLL.  
 DR ZFIN; ZDB-GENE-980526-115; nr2f1.  
 DR InterPro: IPR000536; Hormone\_rec\_lig.  
 DR InterPro: IPR001723; Stdhrmn\_receptor.  
 DR InterPro: IPR001628; znf\_C4steroid.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR ProDom; PD000035; znf\_C4steroid; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 FT Zinc-finger; Vision.  
 FT DNA\_BIND 76 141 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 76 96 C4-TYPE.  
 FT ZN\_FING 112 136 C4-TYPE.  
 FT ZN\_FING 112 136 C4-TYPE.  
 SQ SEQUENCE 411 AA; 45482 MW; B0405FB4EFA0202 CRC64;  
 Query Match 11.0%; Score 71; DB 1; Length 411;  
 Best Local Similarity 26.3%; Pred. No. 3.8;  
 Matches 28; Conservative 14; Mismatches 27; Indels 32; Gaps 6;  
 QY 26 PGVA--RGHRDGRQASRR-----WLOGGQCE-CKDWFLRAPRRKFTVSGLP 71  
 Db 56 PGVAGDKGSGNSGQSQHIECVVGDGKSGKHGYGFTGEGCKSFKRSVRN-LTYTCRA 114  
 QY 72 KQCPDHPFGKGVNKKTRHQRHHRKPNKHSRACQOFLKQC 110  
 Db 115 NRNCPID-----QHRNQCQYCR-----LKKC 136  
 RESULT 6  
 LMB2\_HUMAN  
 ID LMB2\_HUMAN STANDARD; PRT; 1798 AA.  
 AC P55268; Q16321;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Laminin beta-2 chain precursor (S-laminin) (laminin B1s chain).  
 GN LMB2 OR LAMS.  
 OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=95213013; PubMed=7698745;  
Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,  
Champlaud M.F., Burgess R.E., Abrechtsen R.;  
"Human beta 2 chain of laminin (formerly S chain): cDNA cloning,  
chromosomal localization, and expression in carcinomas.";  
Genomics 24:243-252(1994).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=95316263; PubMed=7795887;  
Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,  
Sarioela H., Tryggvason K.;  
"The human laminin beta 2 chain (S-laminin): structure, expression in  
fetal tissues and chromosomal assignment of the LAMB2 gene.";  
Matrix Biol. 14:489-497(1995).  
-!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
is thought to mediate the attachment, migration, and organization  
of cells into tissues during embryonic development by interacting  
with other extracellular matrix components.  
-!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
different polypeptide chains (alpha, beta, gamma), which are bound  
to each other by disulfide bonds into a cross-shaped molecule  
comprising one long and three short arms with globules at each  
end.  
THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
-!- SUBCELLULAR LOCATION: Extracellular.  
-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
CLEFT OF THE NEUROMUSCULAR JUNCTION.  
-!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
-!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
-!- SIMILARITY: Contains 1 laminin N-terminal domain.  
-!- SIMILARITY: Contains 13 laminin EGF-like domains.  
-!- SIMILARITY: Contains 1 laminin IV domain.  
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EMBL; Z68155; CAA92279.1; -  
EMBL; Z68156; CAA92279.1; JOINED.  
EMBL; X79683; CAA56130.1; -  
EMBL; S77512; AAB34692.2; -  
PIR; S53869; S53869.  
HSPG; P02468; IKLO.  
Genew; HGNC:6487; LAMB2.  
MIM; 150325; -  
GO; GO:0005605; C-basal lamina; TAS.  
InterPro; IPR006209; EGF-like.  
InterPro; IPR002049; Laminin\_EGF.  
InterPro; IPR001886; LamNT.  
Pfam; PF00053; laminin\_EGF; 13.  
Pfam; PF00055; laminin\_Nterm; 1.  
PRINTS; PR00011; EGF\_LAMININ.  
SMART; SM00180; EGF\_Lam; 13.  
SMART; SM00136; LamNT; 1.  
PROSITE; PS00022; EGF\_1; 10.  
PROSITE; PS01186; EGF\_2; 2.  
PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
SIGNAL 1 32 POTENTIAL.  
CHAIN 33 1798 LAMININ BETA-2 CHAIN.

FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 283 346 LAMININ EGF-LIKE 1.  
FT DOMAIN 347 409 LAMININ EGF-LIKE 2.  
FT DOMAIN 410 469 LAMININ EGF-LIKE 3.  
FT DOMAIN 470 521 LAMININ EGF-LIKE 4.  
FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).  
FT DOMAIN 553 781 LAMININ DOMAIN IV.  
FT DOMAIN 783 830 LAMININ EGF-LIKE 6.  
FT DOMAIN 831 876 LAMININ EGF-LIKE 7.  
FT DOMAIN 877 926 LAMININ EGF-LIKE 8.  
FT DOMAIN 927 985 LAMININ EGF-LIKE 9.  
FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.  
FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.  
FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.  
FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.  
FT DOMAIN 1190 1409 DOMAIN II.  
FT DOMAIN 1410 1442 DOMAIN I.  
FT DOMAIN 1443 1798 COILED COIL (POTENTIAL).  
FT DOMAIN 1253 1319 COILED COIL (POTENTIAL).  
FT DOMAIN 1472 1526 COILED COIL (POTENTIAL).  
FT DOMAIN 1527 1790 BY SIMILARITY.  
FT DISULFID 283 292 BY SIMILARITY.  
FT DISULFID 285 310 BY SIMILARITY.  
FT DISULFID 312 321 BY SIMILARITY.  
FT DISULFID 324 344 BY SIMILARITY.  
FT DISULFID 347 356 BY SIMILARITY.  
FT DISULFID 349 374 BY SIMILARITY.  
FT DISULFID 377 386 BY SIMILARITY.  
FT DISULFID 389 407 BY SIMILARITY.  
FT DISULFID 410 423 BY SIMILARITY.  
FT DISULFID 412 438 BY SIMILARITY.  
FT DISULFID 440 449 BY SIMILARITY.  
FT DISULFID 452 467 BY SIMILARITY.  
FT DISULFID 470 484 BY SIMILARITY.  
FT DISULFID 472 491 BY SIMILARITY.  
FT DISULFID 493 502 BY SIMILARITY.  
FT DISULFID 505 519 BY SIMILARITY.  
FT DISULFID 783 795 BY SIMILARITY.  
FT DISULFID 785 802 BY SIMILARITY.  
FT DISULFID 804 813 BY SIMILARITY.  
FT DISULFID 816 828 BY SIMILARITY.  
FT DISULFID 831 843 BY SIMILARITY.  
FT DISULFID 833 850 BY SIMILARITY.  
FT DISULFID 852 861 BY SIMILARITY.  
FT DISULFID 864 874 BY SIMILARITY.  
FT DISULFID 877 886 BY SIMILARITY.  
FT DISULFID 879 893 BY SIMILARITY.  
FT DISULFID 896 905 BY SIMILARITY.  
FT DISULFID 908 924 BY SIMILARITY.  
FT DISULFID 927 943 BY SIMILARITY.  
FT DISULFID 929 954 BY SIMILARITY.  
FT DISULFID 956 965 BY SIMILARITY.  
FT DISULFID 968 983 BY SIMILARITY.  
FT DISULFID 986 1000 BY SIMILARITY.  
FT DISULFID 988 1007 BY SIMILARITY.  
FT DISULFID 1010 1019 BY SIMILARITY.  
FT DISULFID 1022 1035 BY SIMILARITY.  
FT DISULFID 1095 1107 BY SIMILARITY.  
FT DISULFID 1097 1114 BY SIMILARITY.  
FT DISULFID 1116 1125 BY SIMILARITY.  
FT DISULFID 1128 1140 BY SIMILARITY.  
FT DISULFID 1143 1155 BY SIMILARITY.  
FT DISULFID 1145 1162 BY SIMILARITY.  
FT DISULFID 1164 1173 BY SIMILARITY.  
FT DISULFID 1176 1187 BY SIMILARITY.  
FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).  
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).  
FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).  
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

Query Match      11.0%; Score 71; DB 1; Length 2262;
Best Local Similarity 26.6%; Pred No. 20;
Matches 29; Conservative 13; Mismatches 31; Indels 36; Gaps 6
13 PLMLSMVSSSLPCVARGHRDEGOAS-----RWLO-----EGGDECE-CK 53
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 PLILPNASKSL-----IEPQHDNAISYEYLTKWKKEISLIERKCFDFFDPELSIFNK 476

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```

Name-Type 1;
  IsoId=P16375-1; Sequence=Displayed;
Name-Type 2;
  IsoId=P16375-1; Sequence=External;
-!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
subfamily.
-----
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; M28663; AAA62770.1; -
EMBL; AE003695; AAF54773.1; -
PIR; A32693; A32693.
HSP; P19793; 2NLL.
TRANSPAC; T02741; -
FlyBase; FBgn0003651; svp.
GO; GO:0005737; P:cytoplasm; IDA.
GO; GO:0007510; P:cardioblast cell fate determination; IEF.
InterPro; IPR000536; Hormone_rec_llg.
InterPro; IPR001723; Stdhmrn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOL1; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger; Vision; Alternative splicing.
DNA_BIND 200 265 NUCLEAR RECEPTOR-TYPE.
ZN_FING 200 220 C4-TYPE.
ZN_FING 236 260 C4-TYPE.
SEQUENCE 543 AA; 57987 MW; 0BC189DCFA1A27213 CRC64;
Query Match 10.9%; Score 70; DB 1; Length 543;
Best Local Similarity 26.7%; Pred. No. 6.4;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;
21 SSSLNPG-----VARGHRDRGQASRRWLQGGQCECKDQWFLRAPRRKFTVSG 69
183 SQSNSGSDSKQNTCEVVGCGDKSGKHGYQFTCEG-----CKSFFKRSVRN-LTYSC 236
70 LPKKQCCDHFKNVKTQRHRRHKNHKSACQFLKQC 110
237 RGSRCNPID-----QHNRNCCQYCR-----LKKC 260
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RESULT 9
IP2_DROME STANDARD; PRT; 746 AA.
P16376;
01-AUG-1990 (Rel. 15, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Steroid receptor seven-up type 2.
SVP OR NR2F3
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
MEDLINE=90124631; PubMed=2105166;
Mlodzik M., Hiromi Y., Weber U., Goodman C.S., Rubin G.M.;

```

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RT "The Drosophila seven-up gene, a member of the steroid receptor gene
superfamily, controls photoreceptor cell fates.";
RL Cell 60:211-224(1990).
CC -!- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
CELLS PRECURSORS DURING EYE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name-Type 2;
CC IsoId=P16376-1; Sequence=Displayed;
CC Name-Type 1;
CC IsoId=P16375-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
subfamily.
-----
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EMBL; M28664; AAA03014.1; -
PIR; B32693; B32693.
HSP; P19793; 2NLL.
FlyBase; FBgn0003651; svp.
InterPro; IPR000536; Hormone_rec_llg.
InterPro; IPR001723; Stdhmrn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOL1; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger; Vision; Alternative splicing.
FT DNA_BIND 200 265 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 200 220 C4-TYPE.
FT ZN_FING 236 260 C4-TYPE.
SQ SEQUENCE 746 AA; 76830 MW; 7F256AFD4165326D CRC64;
Query Match 10.9%; Score 70; DB 1; Length 746;
Best Local Similarity 26.7%; Pred. No. 8.6;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;
21 SSSLNPG-----VARGHRDRGQASRRWLQGGQCECKDQWFLRAPRRKFTVSG 69
183 SQSNSGSDSKQNTCEVVGCGDKSGKHGYQFTCEG-----CKSFFKRSVRN-LTYSC 236
70 LPKKQCCDHFKNVKTQRHRRHKNHKSACQFLKQC 110
237 RGSRCNPID-----QHNRNCCQYCR-----LKKC 260
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RESULT 10
TRBM_HUMAN STANDARD; PRT; 575 AA.
ID TRBM_HUMAN
AC P07204;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Thrombomodulin precursor (Fetomodulin) (TM) (CD141 antigen).
GN THBD OR THRM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

- SEQUENCE FROM N.A.  
MEDLINE=98004395; PubMed=2820710;  
Suzuki K., Kusumoto H., Deyashiki Y., Nishioka J., Maruyama I.,  
Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.;  
"Structure and expression of human thrombomodulin, a thrombin  
receptor on endothelium acting as a cofactor for protein C  
activation.";  
EMBO J. 6:1891-1897(1987).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=88024950; PubMed=2822087;  
Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;  
"Human thrombomodulin: complete cDNA sequence and chromosome  
localization of the gene.";  
Biochemistry 26:4350-4357(1987).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=87317685; PubMed=2819876;  
Jackman R.W., Beeley D.L., Fritze L., Soff G., Rosenberg R.D.;  
"Human thrombomodulin gene is intron depleted: nucleic acid sequences  
of the cDNA and gene predict protein structure and suggest sites of  
regulatory control.";  
Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).  
[4]  
SEQUENCE FROM N.A.  
MEDLINE=88227901; PubMed=2836377;  
Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,  
Deyashiki Y., Maruyama I., Suzuki K.;  
"Gene structure of human thrombomodulin, a cofactor for thrombin-  
catalyzed activation of protein C.";  
J. Biochem. 103:281-285(1988).  
[5]  
SEQUENCE FROM N.A.  
Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
Ozuna M., Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
[6]  
SEQUENCE FROM N.A.  
MEDLINE=21638749; PubMed=11780052;  
Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,  
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
Marsh V.L., Martin S.B., McConachie L.J., McLeay K., McMurray A.A.,  
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
Oliver K., Parker A., Pearce T.A.V., Peck A.I.,  
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
Rogers J.;  
"The DNA sequence and comparative analysis of human chromosome 20.";  
Nature 414:865-871(2001).  
[7]  
CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS.  
MEDLINE=94029900; PubMed=8216207;  
Gerleitz B., Hassell T., Vlahos C.J., Parkinson J.F., Bang N.U.,  
Grinnell B.W.;  
"Identification of the predominant glycosaminoglycan-attachment site  
in soluble recombinant human thrombomodulin: potential regulation of
- RT functionality by glycosyltransferase competition for serine474.";  
Biochem. J. 295:131-140(1993).  
[8]  
RT STRUCTURE BY NMR OF 389-407.  
RX MEDLINE=96007474; PubMed=7559494;  
Adler M., Seto M.H., Nitecki D.E., Lin J.H., Light D.R., Morser J.;  
"The structure of a 19-residue fragment from the C-loop of the fourth  
epidermal growth factor-like domain of thrombomodulin.";  
J. Biol. Chem. 270:23366-23372(1995).  
[9]  
RT STRUCTURE BY NMR OF 364-407.  
RX MEDLINE=96100636; PubMed=8528067;  
Meininger D.P., Hunter M.J., Komives E.A.;  
"Synthesis, activity, and preliminary structure of the fourth  
EGF-like domain of thrombomodulin.";  
Protein Sci. 4:1683-1695(1995).  
[10]  
RT STRUCTURE BY NMR OF 427-444.  
RX MEDLINE=95034791; PubMed=7947766;  
R Srinivasan J., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.;  
"Thrombin-bound structure of an EGF subdomain from human  
thrombomodulin determined by transferred nuclear Overhauser  
effects.";  
Biochemistry 33:13553-13560(1994).  
[11]  
RT STRUCTURE BY NMR OF 427-444.  
RX MEDLINE=96276211; PubMed=8745396;  
Hrabal R., Komives E.A., Ni F.;  
"Structural resiliency of an EGF-like subdomain bound to its target  
protein, thrombin.";  
Protein Sci. 5:195-203(1996).  
[12]  
RT STRUCTURE BY NMR OF 405-444.  
RX MEDLINE=98035729; PubMed=9367781;  
Sampoli Benitez B.A., Hunter M.J., Meininger D.P., Komives E.A.;  
"Structure of the fifth EGF-like domain of thrombomodulin: an  
EGF-like domain with a novel disulfide-bonding pattern.";  
J. Mol. Biol. 273:913-926(1997).  
[13]  
RT VARIANT TED TYR-486.  
RX MEDLINE=95111115; PubMed=7811989;  
Oehlén A.-K., Marlar R.A.;  
"The first mutation identified in the thrombomodulin gene in a  
45-year-old man presenting with thromboembolic disease.";  
Blood 85:330-336(1995).  
[14]  
RT VARIANT TED TYR-486, AND VARIANTS THR-43; ALA-79; SER-495 AND LEU-501.  
RX MEDLINE=97341986; PubMed=9198186;  
Oehlén A.-K., Norlund L., Marlar R.A.;  
"Thrombomodulin gene variations and thromboembolic disease.";  
Thromb. Haemost. 78:396-400(1997).  
[15]  
RT VARIANT VAL-473.  
RX MEDLINE=97206518; PubMed=9157575;  
Norlund L., Holm J., Zoller B., Oehlén A.-K.;  
"A common thrombomodulin amino acid dimorphism is associated with  
myocardial infarction.";  
Thromb. Haemost. 77:248-251(1997).  
[16]  
RT VARIANT THR-43.  
RX MEDLINE=99057299; PubMed=9843165;  
Duggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,  
Stubbs P.J., Manger Cats V., Ireland H.;  
"A mutation in the thrombomodulin gene, 127G to A coding for Ala25Thr,  
and the risk of myocardial infarction in men.";  
Thromb. Haemost. 80:743-748(1998).  
[17]  
RT VARIANT VAL-473.  
RX MEDLINE=21143723; PubMed=11245641;  
Wu K.K., Aleksic N., Ahn C., Boerwinkle E., Folsom A.R.,  
Juneja H.;  
"Thrombomodulin Ala455Val polymorphism and risk of coronary heart  
disease.";

Circulation 103:1386-1389(2001).  
-!- FUNCTION: THROMBOMODULIN IS A SPECIFIC ENDOTHELIAL CELL RECEPTOR THAT FORMS A 1:1 STOICHIOMETRIC COMPLEX WITH THROMBIN. THIS COMPLEX IS RESPONSIBLE FOR THE CONVERSION OF PROTEIN C TO THE ACTIVATED PROTEIN C (PROTEIN CA). ONCE EVOLVED, PROTEIN CA SCISSIONS THE ACTIVATED COFACTORS OF THE COAGULATION MECHANISM, FACTOR VA AND FACTOR VIIIa, AND THEREBY REDUCES THE AMOUNT OF THROMBIN GENERATED.  
-!- SUBCELLULAR LOCATION: Type I membrane protein.  
-!- TISSUE SPECIFICITY: ENDOTHELIAL CELLS ARE UNIQUE IN SYNTHESIZING THROMBOMODULIN.  
-!- POLYMORPHISM: VARIATIONS IN THED ARE ASSOCIATED WITH AN INCREASED RISK OF DEVELOPING THROMBOEMBOLIC DISEASES (TED).  
-!- DISEASE: DEFECTS IN THED COULD BE THE CAUSE OF INHERITED TED, ALSO CALLED INHERITED THROMBOPHILIA. PATIENTS WITH TED HAVE DEFECTS OF THE HAEMOPOIETIC SYSTEM WHICH CREATES A TENDENCY TO THE OCCURRENCE OF THROMBOSIS. TED PLAY AN IMPORTANT ROLE IN THE PATHOGENESIS OF VARIOUS CARDIOVASCULAR DISORDERS.  
-!- SIMILARITY: Contains 6 EGF-like domains.  
-!- DATABASE: NAME=PROW; NOTE=CD guide CD141 entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd141.htm".  
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EMBL; X05495; CAA29045.1; -  
EMBL; M16552; AAB59508.1; -  
EMBL; J02973; AAG61175.1; -  
EMBL; D00210; BAB00149.1; -  
EMBL; AF495471; AAM03232.1; -  
EMBL; AL049651; CAB51954.1; -  
PIR; A41442; THHUB.  
PDB; 1EGT; 15-NOV-95.  
PDB; 1FGD; 20-JUN-96.  
PDB; 1FGE; 20-JUN-96.  
PDB; 1PMR; 08-JUN-95.  
PDB; 1ZAO; 29-JAN-96.  
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Query Match 10.8%; Score 69.5; DB 1; Length 575;  
Best Local Similarity 23.5%; Pred. No. 7.6;  
Matches 24; Conservative 11; Mismatches 26; Indels 41; Gaps 5;  
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5 ISSLLLLLPLMLSMVSSSLNPGVARGHRDGRGQASRW---LQGGQCECKDFLRAPR 61  
209 VGSSAAVPLGLQLMCTAP--PGAVQGHWR-BAPGAWDCSVNGGCEHACN----- 257  
62 RKFTVSGLPKKQCP-----CDHF 80  
258 ----AIPGAPRCQCPAGAAQADGRSCTASATQSCNDLCSEHF 295  
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RESULT 11  
IX3\_CHICK  
SIX3\_CHICK STANDARD; PRT; 314 AA.  
O42406;  
15-DEC-1998 (Rel. 37, Created)  
15-DEC-1998 (Rel. 37, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Homeobox protein SIX3 (Sine oculis homeobox homolog 3) (CSIX3).  
SIX3.  
Gallus gallus (Chicken).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Gallus  
NCBI\_TaxID=9031;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=98168856; PubMed=9510037;  
-----

RA Bovolenta P., Mallamaci A., Puelles L., Boncinelli E.;  
RT "Expression pattern of csix3, a member of the Six/sine oculis family of transcription factors";  
RL Mech. Dev. 70:201-203(1998).  
CC -!- FUNCTION: MAY BE INVOLVED IN VISUAL SYSTEM DEVELOPMENT.  
CC -!- SUBCELLULAR LOCATION: Nuclear (by similarity).  
CC -!- SIMILARITY: BELONGS TO THE SIX/SINE OCULIS HOMEBOX FAMILY.  
-----  
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-----  
EMBL; Y15106; CAA75380.1; -  
DR HSSP; P41778; LDU6  
DR TRANSFAC; T03482; -  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR000047; HTH\_lambdarepressr.  
DR InterPro; IPR007105; SIX.  
DR InterPro; IPR007106; SIX\_SINE\_homeo.  
DR PRINTS; PR00031; HTHREPRESSR.  
DR Pfam; PF00046; homeobox; 1.  
DR PRODOM; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; FALSE\_NEG.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
KW Developmental protein; Homeobox; DNA-binding; Nuclear protein.  
FT DOMAIN 44 50 POLY-GLY.  
FT DNA\_BIND 188 247 HOMEBOX.  
FT DOMAIN 245 248 POLY-ALA.  
SQ SEQUENCE 314 AA; 34677 MW; D9A04530185BA75F CRC64;  
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Query Match 10.7%; Score 69; DB 1; Length 314;  
Best Local Similarity 26.9%; Pred. No. 4.8;  
Matches 25; Conservative 13; Mismatches 33; Indels 22; Gaps 4;  
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QY 41 RWLQGGQCECEC-----KDWFLRAP-----RKFTVSGLPKKQCPGDFHFGNYK 85  
DB 183 RTIWDGQKTHCFKERTSLRLWYLDQPYPNKSKRELAQAATGLTPTQV-----GNWF 236  
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QY 86 KTRHQRRHKPNKHSRACQFLKQCQLRSFALP 118  
DB 237 KNRQRORAAAK-NRLQHOAIGSGMRSLAEP 268  
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RESULT 12  
VDR\_MOUSE  
ID VDR\_MOUSE STANDARD; PRT; 422 AA.  
AC P48281;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).  
GN VDR OR NR11.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95137405; PubMed=7835717;  
RA Kamei Y., Kawada T., Fukuwatari T., Ono T., Kato S., Sugimoto E.;  
RT "Cloning and sequencing of the gene encoding the mouse vitamin D receptor";  
RL Gene 152:281-282(1995).  
CC -!- FUNCTION: Nuclear hormone receptor. VDR mediates the action of vitamin D3 by controlling the expression of hormone sensitive genes.  
CC -!- SUBUNIT: Interacts with NCOA3 and NCOA6 coactivators, leading to a strong increase of transcription of target genes (By similarity).  
-----

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-|- SUBCELLULAR LOCATION: Nuclear.
-|- DOMAIN: Composed of three domains: a modulating N-terminal domain,
a DNA-binding domain and a C-terminal steroid-binding domain.
-|- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
subfamily.

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or send an email to licensed@isb-sib.ch).
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EMBL; D31969; BAA06737.1; .
PIR; PC4019; PC4019.
HSSP; P03372; LHQC.
TRANSFAC; T00883; .
MGD; MGI103076; Vdr.
GO; GO:0006874; P:calcium ion homeostasis; IMP.
GO; GO:0007275; P:development; IMP.
GO; GO:0001501; P:skeletal development; IMP.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zif-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZNF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
zinc-finger; Phosphorylation.
DNA_BIND 24 89 NUCLEAR RECEPTOR-TYPE.
ZNF_FING 24 44 C4-TYPE.
ZNF_FING 60 84 C4-TYPE.
DOMAIN 90 186 HINGE.
DOMAIN 187 422 LIGAND-BINDING.
SEQUENCE 422 AA; 47851 MW; 4704CC8172445732 CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 422;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

50 CE-CKDWFLRAPRRKFTVSGLPKQPCDHFHGNVKKTRHQRHHRKPNKHSRACQQLK 108
41 CEGCKGFFRSMKRKALFT-----CP---FNGDCRITKDNK-----RHCQACR--LK 82

109 QC-----QLRSFAL 117
83 RCVDIGMMKEFIL 95

VDR_XENLA STANDARD; PRT; 422 AA.
O13124;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 39, Last annotation update)
Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
VDR OR NR1L1.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
TISSUE=Kidney;
MEDLINE=97307679; PubMed=9165021;

```

```

RA Li Y.C., Bergwitz C., Jueppner H., Demay M.B.;
RT "Cloning and characterization of the vitamin D receptor from Xenopus
RL laevis.";
CC Endocrinology 138:2347-2353(1997).
CC -|- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -|- SUBCELLULAR LOCATION: Nuclear.
CC -|- TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST
CC LEVEL IN SMALL INTESTINE AND SKIN.
CC -|- DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASES
CC GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE LEVEL
CC SEEN IN ADULT.
CC -|- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licensed@isb-sib.ch).
CC -----
CC EMBL; U91846; AAB58585.1; .
CC DR HSSP; O75469; ILIG.
CC DR InterPro; IPR000536; Hormone_rec_lig.
CC DR InterPro; IPR001723; Stdhrmn_receptor.
CC DR InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zif-C4; 1.
CC DR PRINTS; PR00398; STRDHORMONER.
CC DR PRINTS; PR00047; STROIDFINGER.
CC DR ProDom; PD000035; Znf_C4steroid; 1.
CC DR SMART; SM00430; HOLI; 1.
CC DR SMART; SM00399; ZNF_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNP_BIND 25 90 NUCLEAR RECEPTOR-TYPE.
FT ZNF_FING 25 45 C4-TYPE.
FT ZNF_FING 61 85 C4-TYPE.
FT DOMAIN 91 188 HINGE.
FT DOMAIN 189 422 LIGAND-BINDING.
FT SEQUENCE 422 AA; 48188 MW; C8A9F25414FEE9D5 CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 422;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

50 CE-CKDWFLRAPRRKFTVSGLPKQPCDHFHGNVKKTRHQRHHRKPNKHSRACQQLK 108
42 CEGCKGFFRSMKRKAMFT-----CP---FNGDCRITKDNK-----RHCQSCR--LK 83

109 QC-----QLRSFAL 117
84 RCVDIGMMKEFIL 96

VDR_XENLA STANDARD; PRT; 423 AA.
O13053;
AC 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
GN VDR OR NR1L1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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109 QC---OLRSPAL 117  
:|:|  
> 80 RCVDIGMKKEFIL 92

Search completed: September 13, 2003, 14:44:39  
>b time : 23.3333 secs

un on: September 13, 2003, 14:39:41 ; Search time 50.6667 Seconds  
(without alignments)  
606.084 Million cell updates/sec

correct score: 044  
 1 MKVLISSLLLLPLMLSMV.....SRACQELKOCOLRSFALPL 119  
 sequence:

total number of hits satisfying chosen parameters: 830525

Maximum Match 100%  
Listing first 45 summaries

## SUMMARIES

Description

DT	01-MAR-2003	TREMBLrel. 23,	Last annotation
DI	01 MAR 2003	(TREMBLrel. 23)	Last sequence added

UI-MAR-2003 (TremBLrel. 23, Last sequence update)  
T 01-MAR-2003 (TremBLrel. 23, Last annotation update)

Q83i11 mouse aden

QY	46	GGQCECEKDWFLRAPRR	---KFTVSGLPKKQ---CPCDHFKNVKKTRQRRHHRKPNKHS	100
DB	262	GGPNAESNTTFLRATKRRFFKFIYTSATLPKKQNSTMDNFQKSSVFEDTAHHHNPMDG	321	
QY	101	RACQOFLKQCOL	112	
DB	322	R----	ILKKAPL 329	
RESULT 4				
ID	Q9W745	PRELIMINARY;	PRT; 411 AA.	
AC	Q9W745;			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	COUP	transcription factor 1.		
OS	Xenopus laevis	(African clawed frog).		
OC	Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia;	Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
OC	Xenopodinae;	Xenopus.		
ON	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Langlois M.C., Vanacker J.M., Holland N.D., Escriva H., Queva C.,			
RA	Laudet V., Holland L.Z.			
RT	"AmphicouP-TF, a nuclear orphan receptor of the lancelet Branchiostoma			
RT	floridae, is implicated in retinoic acid signaling pathways."			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.			
DR	EMBL; AF157558; AAD42224.1; -.			
DR	HSSP; P19793; 2NLL.			
DR	InterPro; IPR000536; Hormone_rec.lig.			
DR	InterPro; IPR001723; Stdhrmn_receptor.			
DR	InterPro; IPR001628; Znf_C4steroid.			
DR	Pfam; PF001104; hormone_rec; 1.			
DR	Pfam; PF001105; zf-C4; 1.			
DR	PRINTS; PR00398; STRDHORMONER.			
DR	PRINTS; PR00047; STROIDFINGER.			
DR	ProDom; PD000035; Znf_C4steroid; 1.			
DR	SMART; SM00430; HOLI; 1.			
DR	SMART; SM00399; Znf_C4; 1.			
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.			
KW	DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;			
KW	Transcription regulation; Zinc; Zinc-finger;			
SEQUENCE	411 AA; 45467 MW; 950E285B7FC336FB CRC64;			
Query Match 11.9%; Score 76.5; DB 13; Length 411;				
Best Local Similarity 26.0%; Pred. No. 1.4;				
Matches 26; Conservative 16; Mismatches 25; Indels 33; Gaps 6				
QY	26	PGVA--RGHRDQGSRRWLQ-----	EGGQECE-CKDWFLRAPRRKFMVWSGL 70	
DB	53	PGAAGDKGGGSGQQQHIECVCGDKSSSKHHGQQTCEGCKSFRRSVRRN-LIYTCR 111		
QY	71	PKKQCPDHFKNVKKTRQRRHHRKPNKHSRACQOFLKQC	110	
DB	112	ANRNCPID-----	QHRRNQCCYCR-----LKKC 134	
RESULT 5				
ID	Q8NAP3	PRELIMINARY;	PRT; 752 AA.	
AC	Q8NAP3;			
DT	01-OCT-2002	(TREMBLrel. 22, Created)		
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Hypothetical protein FLJ35036	(Fragment).		
OS	Homo sapiens	(Human).		
OC	Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia;	Eutheria; Primates; Catarrhini; Hominidae; Homo.		
ON	NCBI_TaxID=9606;			





[illegible][illegible]

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
Merkulov G., Milshina N.V., Mobaraj C., Morris J., Moshrefi A.,  
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Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,  
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
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Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
"The genome sequence of *Drosophila melanogaster*,"  
Science 287:2185-2195(2000).  
[2]  
SEQUENCE FROM N.A.  
Celnikier S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
Carlson J.W., Center A., Chape M., Davenport L.B., Dietz S.M.,  
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
Ibezawam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,  
"Sequencing of *Drosophila melanogaster* genome,"  
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
Tupy J.L., Bergman C., Bernier B., Carlson J.W., Celnikier S.E.,  
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,  
"Annotation of *Drosophila melanogaster* genome,"  
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[4]  
SEQUENCE FROM N.A.  
Adams M.D., Celnikier S.E., Gibbs R.A., Rubin G.M., Venter C.J.,  
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[5]  
SEQUENCE FROM N.A.  
FlyBase:  
Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; AE003448; AAF4516.2; -.  
FlyBase; FBgn0015624; neJ.  
InterPro; IPR000104; Antifreeze1.  
InterPro; IPR001487; Bromodomain.  
InterPro; IPR003101; KIX.  
InterPro; IPR000197; TAZ\_finger.  
InterPro; IPR000433; Znf\_ZZ.  
Pfam; PF00439; bromodomain; 1.  
Pfam; PF02172; KIX; 1.  
Pfam; PF02135; zf-TAZ; 2.  
Pfam; PF00569; Z2; 1.  
PRINTS; PR00308; ANTIFREEZE1.  
PRINTS; PR00503; BROMODOMAIN.  
SMART; SM00291; znf\_ZZ; 1.  
PROSITE; PS00633; BROMODOMAIN\_1; 1.  
PROSITE; PS00633; BROMODOMAIN\_2; 1.  
PROSITE; PS0134; zf-TAZ; 2.  
PROSITE; PS01357; zf\_ZZ\_1; 1.

DR PROSITE; PS0135; zf\_ZZ\_2; 1.  
SQ SEQUENCE 3276 AA; 340728 MW; C9D4611ACBD3918A CRC64;  
Query Match 11.0%; Score 71; DB 5; Length 3276;  
Best Local Similarity 26.7%; Pred. No. 52;  
Matches 23; Conservative 11; Mismatches 30; Indels 22; Gaps 3;  
QY 25 NPGVARGHRDQGASRRWLQGGQCECKDWFARPRKFTVSYGLPKKQCDCDFKGNV 84  
DB 2390 NPQRA-----RKSIQRCICISLAHACQCRDANCRLP-----SCKMKLVV 2429  
QY 85 KTRHQRHHRKPNKHSRACQOFLKQC 110  
DB 2430 QHTKNCK--RKPNGGCPICKQLIALC 2453  
RESULT 11  
Q9SQH1 PRELIMINARY; PRT; 160 AA.  
AC Q9SQH1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Allergen.  
GN ARA H 7.  
OS Arachis hypogaea (Peanut).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;  
OC Arachis.  
OX NCBI\_TaxID-3818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Virginia; TISSUE-Seed;  
RX MEDLINE-99406463; PubMed-10474031;  
RA Kleber-Janke T., Cramer R., Appenzeller U., Schlaak M., Becker W.M.;  
RT "Selective cloning of peanut allergens including profilin and 2S  
albumins, by phage display technology,"  
RL Int. Arch. Allergy Immunol. 119:265-274(1999).  
DR EMBL; AF091737; AAB56719.1; -.  
DR InterPro; IPR003612; AAI.  
DR Pfam; PF00234; trypt\_alpha\_amy1; 1.  
DR SMART; SM00499; AAI; 1.  
SQ SEQUENCE 160 AA; 18417 MW; 9F9E4CEB6808D4C CRC64;  
Query Match 10.9%; Score 70.5; DB 10; Length 160;  
Best Local Similarity 22.1%; Pred. No. 2.6;  
Matches 33; Conservative 19; Mismatches 46; Indels 51; Gaps 6;  
QY 1 MKVLISILLLLPLMLSMVSSSLNPGVARGHRDQGASRRWLQGGQCECKDWFAR 60  
DB 1 MMVKLSILVALLGALLVVASATRWDP-----DRSGSRWDAPSRGDDQCORQLQRAN 53  
QY 61 RKFTVSYGLPKKQPC-DHFKNVKKTRHQRHHRKP-----NKHSRAC 103  
DB 54 LR-----PCEHMRVRVEQEQEQEQDEPYPSRSGRGRQPGESDENQRCC 100  
QY 104 Q-----QFLKQ-CQLRSFALP 118  
DB 101 NELNRFQNQRCMCQALQQILQNCQFWVP 129  
RESULT 12  
Q96UA3 PRELIMINARY; PRT; 1290 AA.  
AC Q96UA3;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Hypothetical 137.8 kDa protein.  
GN B11B22.060.  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;



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Query Match      10.9%; Score 70; DB 5; Length 746;
Best Local Similarity 26.7%; Pred. No. 15;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

21  SSSLNPG-----VARGHSDRQASRRWLQGGQCECKDFLAPRRKEMTVSG 69
183  SSSNSGSOIDSQNIQECVCGDKSSKHVQGTCEG-----CKEFFXSVERN-LTISC 236

70  LPKQCPDHFHGNVKKTRHQRHHRKPNKFSRACQFLKQC 110
237  RGRNRCIPD-----QHNRNQCQCR-----LKKC 260

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PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2,7e-62;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MKVLISLLLLPLMLSMYSSSLNPGVARGHSDRGQASRRNLQEGGQCECKDWFLRAP 60  
|||||  
1 MKVLISLLLLPLMLSMYSSSLNPGVARGHSDRGQASRRNLQEGGQCECKDWFLRAP 60  
|||||  
61 RRKMTVSGLPKQPCDHFHKGKGNVKKTRHQRHRRKPNKHSRACQQLKQCLRSFALPL 119  
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61 RRKMTVSGLPKQPCDHFHKGKGNVKKTRHQRHRRKPNKHSRACQQLKQCLRSFALPL 119  
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RESULT 2

3-09-989-723-165  
Sequence 165, Application US/09989723  
Patent No. US20020072092A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gexitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grima, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
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PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16



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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
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; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLLPLMLMSYSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
Db 1 MKVLISLLLLLPLMLMSYSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60

QY 61 RRKFTWYSGLPKKQCPDHFKNVKKTRQHRHRRPNKHSRACQFLKQCOLRSFALPL 119
Db 61 RRKFTWYSGLPKKQCPDHFKNVKKTRQHRHRRPNKHSRACQFLKQCOLRSFALPL 119

RESULT 3
US-09-989-279-165
; Sequence 165, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24

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6	PRIOR APPLICATION NUMBER: 60/089600	
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67	PRIOR FILING DATE: 1998-07-02	
68	PRIOR APPLICATION NUMBER: 60/091544	
69	PRIOR FILING DATE: 1998-07-01	

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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match      100.0%  Score 644;  DB 9;  Length 119;
Best Local Similarity 100.0%  Pred No. 2,7e-62;
Matches 119;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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:~SULT 4
:~09-989-727-165
Sequence 165, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gieritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09  
Query Match 100.0%; Score 644; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2.7e-62;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MKVLISLLILLPLMLMSVSSSLNPGVARGHRRDRGQASRRWLQEGGQCECKDWFLRAP 60  
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QY 61 RRKFTVSGLPKQPCDHEKFGNVKKTTRHORHRRKNKHSRACQQLKQCQLRSFALPL 119  
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RESULT 5

US-09-989-731-165  
; Sequence 165, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC70  
; CURRENT APPLICATION NUMBER: US/09/989,731  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR FILING DATE: 1998-04-28

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PRIOR FILING DATE:	1998-07-02

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.08; Score 644; DB 10; Length 119;  
Best Local Similarity 100.08; Pred. No. 2.7e-62;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ESULT 6  
S-09-989-732-165  
Sequence 165, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavik, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%   Score 644:   DB 10:   Length 119;
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Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J.-Christophe
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-06-02

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70	PRIOR APPLICATION NUMBER: 60/091982	
71	PRIOR FILING DATE: 1998-07-07	
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Query Match 100.0%; Score 644; DB 10; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2,7e-62;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## SULT 8

-09-990-442-165

Sequence 165, Application US/09990442

Patent No. US20020132252A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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TITLE OF INVENTION: Acids Encoding the Same  
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CURRENT FILING DATE: 2001-11-14  
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Query Match 100.0%; Score 644; DB 10; Length 119;  
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Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730PLC25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19





## RESULT 12

S-09-989-721-165

Sequence 165, Application US/09989721

Patent No. US20020142961A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavir, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

ACIDS Encoding the Same

FILE OF INVENTION: P27301C55

CURRENT APPLICATION NUMBER: US/09/989,721

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

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PRIOR FILING DATE: 1998-06-04

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6 PRIOR APPLICATION NUMBER: 60/088326  
7 PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2.7e-62;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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b 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDRGQASRRRLWLGEGGCECKDWFRLAP 60  
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b 61 RKFMVSLPKKQPCDFKGNVKKTRHQRHHRKPNKHSRACQFLKQCOLRSFALPL 119

RESULT 13

US-09-992-598-165  
Sequence 165, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botsteins, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paon, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match Best Local Similarity 100.0%; Score 644; DB 10; Length 119;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60  
Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60  
QY 61 RKFMVSGLPKQCPDHFKGNVKKTRHORHHRKPNKHSRACQOFLKQQLRSFALPL 119  
Db 61 RKFMVSGLPKQCPDHFKGNVKKTRHORHHRKPNKHSRACQOFLKQQLRSFALPL 119

RESULT 14  
US-09-989-293A-165  
; Sequence 165, Application US/09899293A  
; Patent No. US20020177154A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/043787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
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PRIOR APPLICATION NUMBER: 60/088326

PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
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Prior Application Number: 60/090431  
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 Prior Filing Date: 1998-06-24  
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 Prior Filing Date: 1998-07-02  
 Prior Application Number: 60/091633  
 Prior Filing Date: 1998-07-02  
 Prior Application Number: 60/091978  
 Prior Filing Date: 1998-07-07  
 Prior Application Number: 60/091982  
 Prior Filing Date: 1998-07-07  
 Prior Application Number: 60/092182  
 Prior Filing Date: 1998-07-09

Query Match 100.0% Score 644; DB 10; Length 119;  
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 b 1 MKVLSSLLLLPLMLSMWSSSLNPGVARGHRDGGASRWLQEGGQCECKDWFRLAP 60  
 y 61 RKKEMTVSLPKKQPCDHFHKGNYKTRHQRHHRKPNKHSRACQFLKQCOLRSFALPL 119  
 b 61 RKKEMTVSLPKKQPCDHFHKGNYKTRHQRHHRKPNKHSRACQFLKQCOLRSFALPL 119

RESULT 15  
 S-09-989-735-165  
 Sequence 165, Application US/0989735  
 Publication No. US20020193299A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
 APPLICANT: Desnovers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: ROY, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C61  
 CURRENT APPLICATION NUMBER: US/09/989,735  
 CURRENT FILING DATE: 2001-11-19  
 Prior Application Number: 60/049787  
 Prior Filing Date: 1997-06-16  
 Prior Application Number: 60/062250  
 Prior Filing Date: 1997-10-17  
 Prior Application Number: 60/065186  
 Prior Filing Date: 1997-11-12  
 Prior Application Number: 60/065311  
 Prior Filing Date: 1997-11-13  
 Prior Application Number: 60/066770  
 Prior Filing Date: 1997-11-24  
 Prior Application Number: 60/075945  
 Prior Filing Date: 1998-02-25  
 Prior Application Number: 60/078910  
 Prior Filing Date: 1998-03-20  
 Prior Application Number: 60/083322  
 Prior Filing Date: 1998-04-28  
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 Prior Filing Date: 1998-06-04  
 Prior Application Number: 60/088326  
 Prior Filing Date: 1998-06-04  
 Prior Application Number: 60/088167  
 Prior Filing Date: 1998-06-05

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33	PRIOR FILING DATE: 1998-07-01
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35	PRIOR FILING DATE: 1998-07-02
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38	PRIOR APPLICATION NUMBER: 60/091519
39	PRIOR FILING DATE: 1998-07-02
40	PRIOR APPLICATION NUMBER: 60/091626
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42	PRIOR APPLICATION NUMBER: 60/091633
43	PRIOR FILING DATE: 1998-07-02
44	PRIOR APPLICATION NUMBER: 60/091978
45	PRIOR FILING DATE: 1998-07-07
46	PRIOR APPLICATION NUMBER: 60/091982
47	PRIOR FILING DATE: 1998-07-07
48	PRIOR APPLICATION NUMBER: 60/092182
49	PRIOR FILING DATE: 1998-07-09

[illegible]

Search completed: September 13, 2003, 14:48:18  
Job time : 23 secs

GenCore version 5.1.6  
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1 protein - protein search, using sw model

in on: September 13, 2003, 14:41:13 ; Search time 18 seconds  
(without alignments)  
279,722 Million cell updates/sec

File: US-09-786-260-1  
Project score: 644  
Sequence: 1 MKVLISLLLLPLMLSMV.....SRACQFLKQCQLRSFALPL 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Aligned: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	74	11.5	629	4	US-09-252-991A-16777
4	73.5	11.4	70	1	US-07-737-736B-3
5	72.5	11.3	724	4	US-09-252-991A-28517
6	72	11.2	689	4	US-09-252-991A-19258
7	70.5	10.9	420	4	US-09-252-991A-27610
8	70	10.9	188	1	US-08-469-427A-11
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12	70	10.9	188	4	US-08-851-896-11
13	70	10.9	188	4	US-09-355-700-57
14	70	10.9	188	4	US-09-431-888-6
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ALIGNMENTS

RESULT 1  
US-09-996-243-165  
; Sequence 165, Application US/09996243  
; Patent No. 647823

GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
; FILE REFERENCE: P2730P1C13  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28

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PRIOR FILING DATE:	1998-06-26
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PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
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PRIOR APPLICATION NUMBER:	60/091519
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PRIOR APPLICATION NUMBER:	60/091626
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
BEST APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 4; le-59; Indels 0; Gaps 0;  
Matches 119; Conservative 0; Mismatches 0;

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SULT 2

-09-252-991A-17301  
Sequence 17301, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17301

LENGTH: 620

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

-09-252-991A-17301

Query Match 13.1%; Score 84.5; DB 4; Length 620;

Best Local Similarity 30.7%; Pred. No. 0.099;

Matches 27; Conservative 11; Mismatches 23; Indels 27; Gaps 4;

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577 RQQRDQ-HRRRPHREGRGQREDOYR 603

SULT 3

-09-252-991A-16777  
Sequence 16777, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16777

LENGTH: 620

TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16777

Query Match 11.5%; Score 74; DB 4; Length 629;  
Best Local Similarity 30.2%; Pred. No. 1.8;

Matches 32; Conservative 10; Mismatches 28; Indels 36; Gaps 7;

24 LNPV-----ARGHRDRGQASR-----WLQEGGQCECKDWFLRAPRRKFMVSGLPK 72

448 VFPGLDLDLRLRHLRHQGRHRLRLRQWLRFEG-----RDERR---SVARLFR 494

73 KQPCDHFKNVKTSHORHHRKPNKHSRACQFLKQCOLRSFALP 118

495 -----HLHG-----VHRLHRSRDRH-RGAPPALEQPARRTGKP 528

RESULT 4

US-07-737-736B-3

Sequence 3, Application US/07737736B

Patent No. 5260199

GENERAL INFORMATION:

APPLICANT: Deluca, Hector F.

APPLICANT: Ross, Troy K.

APPLICANT: Prahll, Jean M.

TITLE OF INVENTION: Method Of Producing

TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,736B

FILING DATE: 19910730

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Schwartz, Carl R.

REGISTRATION NUMBER: 29,437

REFERENCE/DOCKET NUMBER: 96-296-2185-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 414-277-5715

TELEFAX: 414-277-5774

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 70 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Chicken

PUBLICATION INFORMATION:

AUTHORS: McDonnell, Donald P.

AUTHORS: Mangelsdorf, David J.

AUTHORS: Pike, J. W.

AUTHORS: Haussler, Mark R.

AUTHORS: O'Malley, Bert W.

TITLE: Molecular Cloning of Complementary DNA

TITLE: Encoding the Avian Receptor for Vitamin D

JOURNAL: Science

VOLUME: 235

PAGES: 1214-1217





FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 41979CP2  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: human fibrosarcoma  
-08-469-427A-11

Query Match 10.9%; Score 70; DB 1; Length 188;  
Best Local Similarity 28.4%; Pred. No. 1.2;  
Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;  
43 LQGGGCECKDWFRLAPRRKMTVS-GLPKKQCPCDHFKNVKNTRHQRHRRKPKHRSR 101  
116 LEEHSQ-CECR-----PKKDSAVKPDSPRLCP-----RCTQHQRDPDPTC 157  
102 ACQOFLKQCQLRSF 115  
158 RC-----RCRRRSF 166

SUIT 9  
-08-609-443B-11  
Sequence 11, Application US/08609443B  
Patent No. 5840693  
GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: OLOFSSON, Birgitta  
APPLICANT: ALITALO, Kari  
APPLICANT: PAJUSOLA, Katri  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,443B  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/469,427  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/569,063

FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 1064/41979CP4  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: human fibrosarcoma  
US-08-609-443B-11

Query Match 10.9%; Score 70; DB 2; Length 188;  
Best Local Similarity 28.4%; Pred. No. 1.2;  
Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;  
43 LQGGGCECKDWFRLAPRRKMTVS-GLPKKQCPCDHFKNVKNTRHQRHRRKPKHRSR 101  
116 LEEHSQ-CECR-----PKKDSAVKPDSPRLCP-----RCTQHQRDPDPTC 157  
102 ACQOFLKQCQLRSF 115  
158 RC-----RCRRRSF 166

RESULT 10  
US-08-569-063C-11  
Sequence 11, Application US/08569063C  
Patent No. 5928939  
GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: OLOFSSON, Birgitta  
APPLICANT: ALITALO, Kari  
APPLICANT: PAJUSOLA, Katri  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,063C  
FILING DATE: 06-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/469,427  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 1064/41979CP3  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844

[REDACTED]

SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: human fibrosarcoma  
-08-851-896-11

Query Match 10.9%; Score 70; DB 4; Length 188;  
Best Local Similarity 28.4%; Pred. No. 1.2; Indels 24; Gaps 5;  
Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

43 LQGGQCECKDWFRLAPRRKFTVS-GLPKKQCPDHFKNVKKTRHQRHHRKPNKHSR 101  
116 LEEHSQ-CECR-----PKKDSAVKPSRPLCP-----RCTQHQRDPDPTC 157

102 ACQOFLKQCQLRSF 115  
158 RC-----RCRRRSF 166

RESULT 13  
US-09-355-700-57  
Sequence 57, Application US/09355700  
Patent No. 6361946

GENERAL INFORMATION:  
APPLICANT: Ludwig Institute for Cancer Research  
Helsinki University Licensing  
Alitalo, Kari(U.S. only)  
Joukov, Vladimir (U.S. only)

TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/355.700  
FILING DATE: 05-NOV-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/795.430  
FILING DATE: 05-FEB-1997  
APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996  
APPLICATION NUMBER: 08/671.573  
FILING DATE: 28-JUN-1996  
APPLICATION NUMBER: 08/601.132  
FILING DATE: 14-FEB-1996  
APPLICATION NUMBER: 08/585.895  
FILING DATE: 12-JAN-1996  
APPLICATION NUMBER: 08/510.133  
FILING DATE: 01-AUG-1995  
APPLICATION NUMBER: 08/340.011  
FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38.153  
REFERENCE/DOCKET NUMBER: 28967/34140

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-09-355-700-57

Query Match 10.9%; Score 70; DB 4; Length 188;  
Best Local Similarity 28.4%; Pred. No. 1.2; Indels 24; Gaps 5;  
Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

QY 43 LQGGQCECKDWFRLAPRRKFTVS-GLPKKQCPDHFKNVKKTRHQRHHRKPNKHSR 101  
DB 116 LEEHSQ-CECR-----PKKDSAVKPSRPLCP-----RCTQHQRDPDPTC 157

QY 102 ACQOFLKQCQLRSF 115  
DB 158 RC-----RCRRRSF 166

RESULT 14  
US-09-431-888-6  
Sequence 6, Application US/09431888A  
Patent No. 6541008

GENERAL INFORMATION:  
APPLICANT: Wise, Lyn M  
APPLICANT: Mercer, Andrew A  
APPLICANT: Savory, Loreen J  
APPLICANT: Fleming, Stephen B  
APPLICANT: Stackler, Stephen

TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF  
TITLE OF INVENTION: VIRUS N22 BINDS AND ACTIVATES MAMMALIAN VEGF  
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF  
FILE REFERENCE: Sequence Listing for 09/431.833  
Patent No. 6541008  
CURRENT APPLICATION NUMBER: US/09/431.888A  
CURRENT FILING DATE: 1999-11-02  
EARLIER APPLICATION NUMBER: 60/106.689  
EARLIER FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: 60/106.800  
EARLIER FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 6  
LENGTH: 188  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-431-888-6

Query Match 10.9%; Score 70; DB 4; Length 188;  
Best Local Similarity 28.4%; Pred. No. 1.2; Indels 24; Gaps 5;  
Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

QY 43 LQGGQCECKDWFRLAPRRKFTVS-GLPKKQCPDHFKNVKKTRHQRHHRKPNKHSR 101  
DB 116 LEEHSQ-CECR-----PKKDSAVKPSRPLCP-----RCTQHQRDPDPTC 157

QY 102 ACQOFLKQCQLRSF 115  
DB 158 RC-----RCRRRSF 166

RESULT 15  
US-09-252-991A-30510  
Sequence 30510, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.

